

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 12, 2006, 16:10:19 ; Search time 71.5 Seconds  
(without alignments)  
30.726 Million cell updates/sec

Title: US-10-716-030-1

Perfect score: 24

Sequence: 1 LNRRRA 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_21.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003s.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	7	ADI52979	ADI52979 Polysacch
2	24	100.0	11	ABG94362	ABG94362 Human tum
3	24	100.0	11	ABG80698	ABG80698 Human tum
4	24	100.0	11	ADI40738	ADI40738 Human TNF
5	24	100.0	14	ADI19860	ADI19860 TNFalpha
6	24	100.0	14	ADI40811	ADI40811 C-TNF- $\alpha$ P
7	24	100.0	16	ADI19837	ADI19837 TNFalpha
8	24	100.0	16	ADI19839	ADI19839 TNFalpha
9	24	100.0	16	ADI19856	ADI19856 TNFalpha
10	24	100.0	16	ADI19851	ADI19851 TNFalpha
11	24	100.0	16	ADI19833	ADI19833 TNFalpha
12	24	100.0	16	ADI19836	ADI19836 TNFalpha
13	24	100.0	17	ABR42094	ABR42094 Human tum
14	24	100.0	20	AAR05522	AAR05522 Tumour ne
15	24	100.0	21	AAR06807	AAR06807 Tumour ne
16	24	100.0	21	AAR05523	AAR05523 Tumour ne
17	24	100.0	30	AAR06804	AAR06804 Tumour ne
18	24	100.0	30	ADI19844	ADI19844 TNFalpha
19	24	100.0	30	ADI19845	ADI19845 TNFalpha
20	24	100.0	30	ADI19854	ADI19854 TNFalpha
21	24	100.0	30	ADI19847	ADI19847 TNFalpha
22	24	100.0	30	ADI19850	ADI19850 TNFalpha
23	24	100.0	30	ADI19858	ADI19858 TNFalpha
24	24	100.0	30	ADI19832	ADI19832 TNFalpha

25 24 100.0 30 6 ADA19827  
26 24 100.0 30 6 ADA19841  
27 24 100.0 30 7 ADK41113  
28 24 100.0 31 6 ADA19830  
29 24 100.0 31 6 ADA19849  
30 24 100.0 31 6 ADA19857  
31 24 100.0 31 6 ADA19838  
32 24 100.0 32 8 ABO58737  
33 24 100.0 35 7 ADK41079  
34 24 100.0 36 3 AAB38436  
35 24 100.0 51 4 AAE13097  
36 24 100.0 51 5 AAG66035  
37 24 100.0 51 8 ADL16846  
38 24 100.0 51 8 ADU64356  
39 24 100.0 52 8 ADJ36285  
40 24 100.0 69 3 AAG01730  
41 24 100.0 70 5 ABP34565  
42 24 100.0 80 8 ADX72124  
43 24 100.0 87 5 ABP34953  
44 24 100.0 88 4 AAU52620  
45 24 100.0 88 6 ABM49139

RESULT 1  
ADI52979

ID ADI52979 standard; peptide; 7 AA.

XX AC ADI52979;

XX DT 06-MAY-2004 (first entry)

XX DE Polysaccharide binding (PB) peptide #15.

XX KW Drug delivery; polysaccharide binding; PB.

XX OS Unidentified.

XX PN US2003190364-A1.

XX PD 09-OCT-2003.

XX PF 01-APR-2003; 2003US-00405339.

XX PR 01-APR-2002; 2002US-0369568P.

XX PA (PANI/) PANITCH A.

XX PA (SEAL/) SEAL B.

XX PI Panitch A, Seal B;

XX DR WPI; 2004-069109/07.

XX XX Composition useful for releasing therapeutic agent comprises a polymer network, several polysaccharide binding polypeptides bound to the polymer network and negatively charged polysaccharides bound to the polypeptides.

XX PS Claim 9; SEQ ID NO 40; 33pp; English.

XX CC The present invention provides compositions for drug delivery, comprising a polymer network, several polysaccharide binding (PB) polypeptides and negatively charged polysaccharides. The present sequence is

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 24; DB 8; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5

ALIGNMENTS

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Db          1 LNRRRA 5
          |||||
RESULT 2
ABG94362
ID ABG94362 standard; peptide; 11 AA.
XX
AC ABG94362;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human tumour necrosis factor (TNF) epitope #2.
XX
KW Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
KW cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
KW vaccine; infectious disease.
XX
OS Homo sapiens.
XX
PN WO200256905-A2.
XX
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002WO-IB000166.
XX
PR 19-JAN-2001; 2001US-0262379P.
PR 04-MAY-2001; 2001US-0288549P.
PR 05-OCT-2001; 2001US-0326998P.
PR 07-NOV-2001; 2001US-0331045P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;
PI Piossek C;
XX
XX WPI; 2002-627351/67.
XX
DR Molecular antigen array used in the production of vaccines for infectious
PT diseases.
XX
PS Disclosure; Page 82; 441pp; English.
XX
CC This invention relates to a novel ordered and repetitive antigen array
CC used in the production of vaccines for infectious diseases. The invention
CC also discloses a composition comprising a non-natural molecular scaffold
CC comprising a core particle selected from a core particle of a non-natural
CC origin and a core particle of natural origin and an organiser comprising
CC at least one first attachment site, where the organiser is connected to
CC the core particle by at least one covalent bond. Also disclosed is an
CC antigen or antigenic determinant with at least one second attachment
CC site, where the antigen or antigenic determinant is amyloid beta peptide
CC (Abetal-42) or its fragment and where the second attachment site is
CC selected from an attachment site not naturally occurring with the antigen
CC or antigenic determinant and an attachment site naturally occurring with
CC the antigen or antigenic determinant, where the second attachment site is
CC capable of association through at least one non-peptide bond to the first
CC attachment site and where the antigen or antigenic determinant and the
CC scaffold interact through the association to form an ordered and
CC repetitive antigen array. The invention also comprises a coat protein
CC capable of forming a capsid which comprises mutant Qbeta coat proteins
CC having an amino acid sequence selected from five amino acid sequences
CC fully defined in the specification. The compounds of the invention may
CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
CC immunisation and as a vaccine. The present sequence represents a protein
CC sequence used to create the compositions of the invention
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 24; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY          1 LNRRRA 5
          |||||
Db          5 LNRRRA 9
          |||||
RESULT 3
ABG80698
ID ABG80698 standard; peptide; 11 AA.
XX
AC ABG80698;
XX
DT 29-NOV-2002 (first entry)
XX
DE Human tumour necrosis factor 22-32 epitope.
XX
KW Molecular antigen array; vaccine; antigen; antimicrobial;
KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;
KW graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;
KW adult respiratory distress syndrome; ARDS; Crohn's disease;
KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
KW Grave's disease; systemic lupus erythematosus; osteoporosis;
KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;
KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
KW enterokinase; cysteine-containing linker.
XX
OS Homo sapiens.
XX
PN WO200256907-A2.
XX
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002WO-IB000168.
XX
PR 19-JAN-2001; 2001US-0262379P.
PR 04-MAY-2001; 2001US-0288549P.
PR 05-OCT-2001; 2001US-0326998P.
PR 07-NOV-2001; 2001US-0331045P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (NOVS ) NOVARTIS PHARMA AG.
PA (MAUR/) MAURER P.
PA (LECH/) LECHNER F.
PA (ORTW/) ORTMANN R.
PA (LUEO/) LUEOEND R.
PA (STAU/) STAUFENBIEL M.
PA (FREY/) FREY P.
XX
PI Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;
PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
XX
XX WPI; 2002-636514/68.
XX
DR Molecular antigen array used in the production of vaccines for infectious
PT diseases.
XX
PS Disclosure; Page 82; 418pp; English.
XX
CC The invention relates to a composition comprising: (a) a non-natural
CC molecular scaffold comprising: (i) a core particle selected from: (1) a
CC core particle of a non-natural origin; and (2) a core particle of natural
CC origin; and (ii) an organiser comprising at least one first attachment
CC site, where the organiser is connected to the core particle by at least
CC one covalent bond; (b) an antigen or antigenic determinant with at least
CC one second attachment site, where the antigen or antigenic determinant is
CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
CC attachment site is selected from: (i) an attachment site not naturally
CC occurring with the antigen or antigenic determinant; and (ii) an
CC attachment site naturally occurring with the antigen or antigenic
CC determinant, where the second attachment site is capable of association
CC through at least one non-peptide bond to the first attachment site; and

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CC where the antigen or antigenic determinant and the scaffold interact  
 CC through the association to form an ordered and repetitive antigen array.  
 CC Also included is a process for producing a non-naturally occurring  
 CC ordered and repetitive antigen array. The composition is used in  
 CC immunisation and as a vaccine for diseases such as influenza, graft  
 CC versus host disease, IGE-mediated allergic reactions, anaphylaxis, adult  
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,  
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,  
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia  
 CC gravis, immunoproliferative disease lymphadenopathy,  
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,  
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,  
 CC osteoporosis and infectious diseases. The present sequence is an antigen  
 CC for use in the array of the invention. The antigen is modified to possess  
 CC a cleavage site (enterokinase or factor Xa) and a Cysteine- containing N-  
 CC or C-terminal linker peptide which serves as the attachment point to a  
 CC virus like particle or bacterial protein (the scaffold protein)  
 XX  
 SQ Sequence 11 AA;

Query Match 100.0%; Score 24; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
 Db |||||  
 5 LNRRRA 9

RESULT 4  
 ADI40738  
 ID ADI40738 standard; peptide; 11 AA.

AC ADI40738;

XX 22-APR-2004 (first entry)

XX Human TNF-alpha peptide SEQ ID NO:29.

XX virus-like particle; bacteriophage AP205; coat protein; cytostatic;  
 KW vaccine; gene therapy; cancer; allergy; asthma; TNF-alpha.

XX Homo sapiens.

XX WO2004007538-A2.

XX 22-JAN-2004.

XX 14-JUL-2003; 2003WO-BF007572.

XX 17-JUL-2002; 2002US-0396126P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann MF, Tissot A, Pumpens P, Cielens I, Renhofa R;

XX WPI; 2004-122882/12.

XX New virus-like particle, useful for preparing a composition for treating  
 PT or preventing a disease e.g., cancer, allergy or asthma.

XX Disclosure; SEQ ID NO 29; 170pp; English.

XX The present invention describes a virus-like particle (I) which  
 CC comprises: (a) a protein having the 131-amino acid sequence of  
 CC bacteriophage AP205 coat protein or the mutant coat protein, see ADI40710  
 CC or ADI40712 respectively; or (b) a mutein of the protein of (a). Also  
 CC described: (1) a mutein of the recombinant protein having the 131-amino  
 CC acid sequence; (2) a vector for producing a AP205 virus like particle  
 CC comprising a nucleotide sequence being at least 80, 90, 95 or 99%  
 CC identical to that of the sequence comprising 3635 or 3613 bp or producing  
 CC a recombinant protein comprising a nucleotide sequence encoding a  
 CC polypeptide fused to a protein; (3) a pharmaceutical composition

CC comprising the composition and a carrier; (4) a process for producing a  
 CC non-naturally occurring, ordered and repetitive antigen array; (5) a  
 CC method of treating or preventing a disease, disorder or physiologic  
 CC conditions in an individual; (6) a nucleic acid molecule comprising 3635-  
 CC bp sequence; (7) a host cell containing a nucleic acid or a vector; and  
 CC (8) a method of producing the virus-like particle. (I) has cytostatic  
 CC activity, and can be used in vaccines, and in gene therapy. The virus-  
 CC like particle is useful for preparing a composition for treating or  
 CC preventing a disease e.g., cancer, allergy or asthma. The present  
 CC sequence represents a TNF-alpha peptide, which is used in the  
 CC exemplification of the present invention.

XX Sequence 11 AA;

Query Match 100.0%; Score 24; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
 Db |||||  
 5 LNRRRA 9

RESULT 5

ADA19860

ID ADA19860 standard; peptide; 14 AA.

XX ADA19860;

XX 20-NOV-2003 (first entry)

XX TNFalpha receptor binding peptide SEQ ID NO:34.

XX molecular library; identification; detection; binding site;  
 KW tumour necrosis factor alpha; TNFalpha; protein-protein interaction;  
 KW protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;  
 KW TNFalpha receptor; tumour necrosis factor alpha receptor;  
 KW inflammatory disease; Crohn's disease; intestinal ulceration;  
 KW intestinal irritation.

XX Synthetic.

XX EP1279962-A1.

XX 29-JAN-2003.

XX 27-JUL-2001; 2001EP-00202879.

XX 27-JUL-2001; 2001EP-00202879.

XX (PEPS-) PEPSAN SYSTEMS BV.

XX Slootstra JW, Puijk WC, Van Dijk E;

XX WPI; 2003-259178/26.

XX Producing molecular library for identifying binding site of tumor  
 PT necrosis factor-alpha, comprises providing the library with many  
 PT molecules produced by segmental linkage of nucleic acids or peptides.

XX Disclosure; Page 22; 70pp; English.

XX The present invention describes a method (M1) for producing a molecular  
 CC library for identifying or detecting a binding site of tumour necrosis  
 CC factor alpha (TNFalpha). (M1) comprises providing the library with  
 CC several molecules, and further generating at least one of the molecules  
 CC by linking a first segment to a second segment. Also described: (1) a  
 CC library (I) comprising several molecules comprising at least a first and  
 CC a second segment obtainable by (M1); (2) a solid support (II) comprising  
 CC (I); (3) a synthetic or binding molecule (III) comprising a binding site  
 CC identifiable or obtainable by using (I); and (4) determining (M2) a  
 CC minimally essential motif for a binding site, by generating a library of  
 CC test molecules, determining the binding activity of a binding molecule

CC with the test molecules, calculating the average binding activity of test  
 CC molecules present in the library comprising a certain motif, and  
 CC determining a motif with a high average binding activity of test  
 CC molecules comprising the motif. (M1) is useful for producing a molecular  
 CC library for identifying or detecting a binding site of TNFalpha. (I) is  
 CC useful for screening for a binding site of TNFalpha capable of  
 CC interacting with a binding molecule, by screening a library with at least  
 CC one potential binding molecule and detecting binding between a member of  
 CC the library and the potential binding molecule. The binding molecule  
 CC comprises a hTNFalpha-2 receptor, and the binding site is a discontinuous  
 CC binding site. (I) and (II) are useful for identifying or obtaining a  
 CC synthetic molecule comprising a binding site of hTNFalpha, or a binding  
 CC molecule capable of binding to a binding site of hTNFalpha. (III) is  
 CC useful for interfering with or effecting binding to a binding molecule of  
 CC hTNFalpha. The molecular libraries produced by (M1) are useful for  
 CC detecting or screening for discontinuous binding sites, in particular in  
 CC relation to binding molecule-ligand interactions such as for e.g. protein  
 CC -protein, protein-nucleic acid and nucleic acid-nucleic acid  
 CC interactions. The identified peptide constructs are useful to develop new  
 CC ligands with agonistic or antagonistic activity for human TNFalpha  
 CC receptor action and are useful in control and prevention of an array of  
 CC diseases with (chronic) inflammatory components such as Crohn's disease  
 CC and other intestinal ulcerations or irritations. The present sequence  
 CC represents a TNFalpha receptor binding peptide which is used in the  
 CC exemplification of the present invention.

XX Sequence 14 AA;

Query Match 100.0%; Score 24; DB 6; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
 Db |||||  
 7 LNRRRA 11

RESULT 6  
 ADI40811  
 ID ADI40811 standard; peptide; 14 AA.

XX AC ADI40811;

XX DT 22-APR-2004 (first entry)

XX DE C-TNF-alpha peptide mutant SEQ ID NO:102.

XX KW virus-like particle; bacteriophage AP205; coat protein; cytostatic;  
 KW vaccine; gene therapy; cancer; allergy; asthma; TNF-alpha; mutant.

XX OS Synthetic.

XX PN WO2004007538-A2.

XX PD 22-JAN-2004.

XX PF 14-JUL-2003; 2003WO-EP007572.

XX PR 17-JUL-2002; 2002US-0396126P.

XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX PI Bachmann MF, Tissot A, Pumpens P, Cielens I, Renhofs R;

XX DR WPI; 2004-122882/12.

XX PT New virus-like particle, useful for preparing a composition for treating  
 PT or preventing a disease e.g., cancer, allergy or asthma.

XX PS Disclosure; SEQ ID NO 102; 170pp; English.

XX CC The present invention describes a virus-like particle (I) which  
 CC comprises: (a) a protein having the 131-amino acid sequence of

CC bacteriophage AP205 coat protein or the mutant coat protein, see ADI40710  
 CC or ADI40712 respectively; or (b) a mutant of the protein of (a). Also  
 CC described: (1) a mutant of the recombinant protein having the 131-amino  
 CC acid sequence; (2) a vector for producing a AP205 virus like particle  
 CC comprising a nucleotide sequence being at least 80, 90, 95 or 99%  
 CC identical to that of the sequence comprising 3635 or 3613 bp or producing  
 CC a recombinant protein comprising a nucleotide sequence encoding a  
 CC polypeptide fused to a protein; (3) a pharmaceutical composition  
 CC comprising the composition and a carrier; (4) a process for producing a  
 CC non-naturally occurring, ordered and repetitive antigen array; (5) a  
 CC method of treating or preventing a disease, disorder or physiologic  
 CC conditions in an individual; (6) a nucleic acid molecule comprising 3635-  
 CC bp sequence; (7) a host cell containing a nucleic acid or a vector; and  
 CC (8) a method of producing the virus-like particle. (I) has cytostatic  
 CC activity, and can be used in vaccines, and in gene therapy. The virus-  
 CC like particle is useful for preparing a composition for treating or  
 CC preventing a disease e.g., cancer, allergy or asthma. The present  
 CC sequence represents a TNF-alpha mutant peptide, which is used in the  
 CC exemplification of the present invention.

XX Sequence 14 AA;

Query Match 100.0%; Score 24; DB 8; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
 Db |||||  
 8 LNRRRA 12

RESULT 7  
 ADA19837  
 ID ADA19837 standard; peptide; 16 AA.

XX AC ADA19837;

XX DT 20-NOV-2003 (first entry)

XX DE TNFalpha receptor binding peptide SEQ ID NO:11.

XX KW molecular library; identification; detection; binding site;  
 KW tumour necrosis factor alpha; TNFalpha; protein-protein interaction;  
 KW protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;  
 KW TNFalpha receptor; tumour necrosis factor alpha receptor;  
 KW inflammatory disease; Crohn's disease; intestinal ulceration;  
 KW intestinal irritation.

XX OS Synthetic.

XX PN EP1279962-A1.

XX PD 29-JAN-2003.

XX PF 27-JUL-2001; 2001EP-00202879.

XX PR 27-JUL-2001; 2001EP-00202879.

XX PA (PEPS-) PEPSCAN SYSTEMS BV.

XX PI Slootstra JW, Puijk WC, Van Dijk E;

XX DR WPI; 2003-259178/26.

XX PT Producing molecular library for identifying binding site of tumor  
 PT necrosis factor-alpha, comprises providing the library with many  
 PT molecules produced by segmental linkage of nucleic acids or peptides.

XX PS Disclosure; Page 16; 70pp; English.

XX CC The present invention describes a method (M1) for producing a molecular  
 CC library for identifying or detecting a binding site of tumour necrosis  
 CC factor alpha (TNFalpha). (M1) comprises providing the library with

CC several molecules, and further generating at least one of the molecules  
 CC by linking a first segment to a second segment. Also described: (1) a  
 CC library (I) comprising several molecules comprising at least a first and  
 CC a second segment obtainable by (M1); (2) a solid support (II) comprising  
 CC (I); (3) a synthetic or binding molecule (III) comprising a binding site  
 CC identifiable or obtainable by using (I); and (4) determining (M2) a  
 CC minimally essential motif for a binding site, by generating a library of  
 CC test molecules, determining the binding activity of a binding molecule  
 CC with the test molecules, calculating the average binding activity of test  
 CC molecules present in the library comprising a certain motif, and  
 CC determining a motif with a high average binding activity of test  
 CC molecules comprising the motif. (M1) is useful for producing a molecular  
 CC library for identifying or detecting a binding site of TNFalpha. (I) is  
 CC useful for screening for a binding site of TNFalpha capable of  
 CC interacting with a binding molecule, by screening a library with at least  
 CC one potential binding molecule and detecting binding between a member of  
 CC the library and the potential binding molecule. The binding molecule  
 CC comprises a hTNFalpha-2 receptor, and the binding site is a discontinuous  
 CC synthetic molecule comprising a binding site of hTNFalpha. (III) is  
 CC molecule capable of binding to a binding site of hTNFalpha. (III) is  
 CC useful for interfering with or effecting binding to a binding molecule of  
 CC hTNFalpha. The molecular libraries produced by (M1) are useful for  
 CC detecting or screening for discontinuous binding sites, in particular in  
 CC relation to binding molecule-ligand interactions such as for e.g. protein  
 CC -protein, protein-nucleic acid and nucleic acid-nucleic acid  
 CC interactions. The identified peptide constructs are useful to develop new  
 CC ligands with agonistic or antagonistic activity for human TNFalpha  
 CC receptor action and are useful in control and prevention of an array of  
 CC diseases with (chronic) inflammatory components such as Crohn's disease  
 CC and other intestinal ulcerations or irritations. The present sequence  
 CC represents a TNFalpha receptor binding peptide which is used in the  
 CC exemplification of the present invention.

XX SQ Sequence 16 AA;

Query Match 100.0%; Score 24; DB 6; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNRRRA 5  
 |||||  
 Db 9 LNRRRA 13

RESULT 8  
 ADA19839  
 ID ADA19839 standard; peptide; 16 AA.

XX AC ADA19839;

XX DT 20-NOV-2003 (first entry)

XX XX TNFalpha receptor binding peptide SEQ ID NO:13.

XX molecular library; identification; detection; binding site;  
 XX tumour necrosis factor alpha; TNFalpha; protein-protein interaction;  
 XX protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;  
 XX TNFalpha receptor; tumour necrosis factor alpha receptor;  
 XX inflammatory disease; Crohn's disease; intestinal ulceration;  
 XX intestinal irritation.

XX OS Synthetic.

XX PN EP1279962-A1.

XX XX 29-JAN-2003.

XX XX 27-JUL-2001; 2001EP-00202879.

XX XX 27-JUL-2001; 2001EP-00202879.

XX XX (PEPS-) PEPSCAN SYSTEMS BV.

XX Sloutstra JW, Puijk WC, Van Dijk E;  
 PI WPI; 2003-259178/26.

XX Producing molecular library for identifying binding site of tumor  
 PT necrosis factor-alpha, comprises providing the library with many  
 PT molecules produced by segmental linkage of nucleic acids or peptides.

XX Disclosure; Page 17; 70pp; English.

XX The present invention describes a method (M1) for producing a molecular  
 CC library for identifying or detecting a binding site of tumour necrosis  
 CC factor alpha (TNFalpha). (M1) comprises providing the library with  
 CC several molecules, and further generating at least one of the molecules  
 CC by linking a first segment to a second segment. Also described: (1) a  
 CC library (I) comprising several molecules comprising at least a first and  
 CC a second segment obtainable by (M1); (2) a solid support (II) comprising  
 CC (I); (3) a synthetic or binding molecule (III) comprising a binding site  
 CC identifiable or obtainable by using (I); and (4) determining (M2) a  
 CC minimally essential motif for a binding site, by generating a library of  
 CC test molecules, determining the binding activity of a binding molecule  
 CC with the test molecules, calculating the average binding activity of test  
 CC molecules present in the library comprising a certain motif, and  
 CC determining a motif with a high average binding activity of test  
 CC molecules comprising the motif. (M1) is useful for producing a molecular  
 CC library for identifying or detecting a binding site of TNFalpha. (I) is  
 CC useful for screening for a binding site of TNFalpha capable of  
 CC interacting with a binding molecule, by screening a library with at least  
 CC one potential binding molecule and detecting binding between a member of  
 CC the library and the potential binding molecule. The binding molecule  
 CC comprises a hTNFalpha-2 receptor, and the binding site is a discontinuous  
 CC synthetic molecule comprising a binding site of hTNFalpha. (III) is  
 CC molecule capable of binding to a binding site of hTNFalpha. (III) is  
 CC useful for interfering with or effecting binding to a binding molecule of  
 CC hTNFalpha. The molecular libraries produced by (M1) are useful for  
 CC detecting or screening for discontinuous binding sites, in particular in  
 CC relation to binding molecule-ligand interactions such as for e.g. protein  
 CC -protein, protein-nucleic acid and nucleic acid-nucleic acid  
 CC interactions. The identified peptide constructs are useful to develop new  
 CC ligands with agonistic or antagonistic activity for human TNFalpha  
 CC receptor action and are useful in control and prevention of an array of  
 CC diseases with (chronic) inflammatory components such as Crohn's disease  
 CC and other intestinal ulcerations or irritations. The present sequence  
 CC represents a TNFalpha receptor binding peptide which is used in the  
 CC exemplification of the present invention.

XX SQ Sequence 16 AA;

Query Match 100.0%; Score 24; DB 6; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNRRRA 5  
 |||||  
 Db 4 LNRRRA 8

RESULT 9

ADA19856

ID ADA19856 standard; peptide; 16 AA.

XX AC ADA19856;

XX DT 20-NOV-2003 (first entry)

XX XX TNFalpha receptor binding peptide SEQ ID NO:30.

XX molecular library; identification; detection; binding site;

XX tumour necrosis factor alpha; TNFalpha; protein-protein interaction;

XX protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;

XX TNFalpha receptor; tumour necrosis factor alpha receptor;

KW inflammatory disease; Crohn's disease; intestinal ulceration;  
 XX intestinal irritation.

OS Synthetic.

XX EP1279962-A1.

XX 29-JAN-2003.

XX 27-JUL-2001; 2001EP-00202879.

XX 27-JUL-2001; 2001EP-00202879.

XX (PEPS-) PEPSCAN SYSTEMS BV.

XX Slootstra JW, Puijk WC, Van Dijk E;

XX WPI; 2003-259178/26.

XX Producing molecular library for identifying binding site of tumor  
 PT necrosis factor-alpha, comprises providing the library with many  
 PT molecules produced by segmental linkage of nucleic acids or peptides.

XX Disclosure; Page 21; 70pp; English.

XX The present invention describes a method (M1) for producing a molecular  
 CC library for identifying or detecting a binding site of tumour necrosis  
 CC factor alpha (TNFalpha). (M1) comprises providing the library with  
 CC several molecules, and further generating at least one of the molecules  
 CC by linking a first segment to a second segment. Also described: (1) a  
 CC library (I) comprising several molecules comprising at least a first and  
 CC a second segment obtainable by (M1); (2) a solid support (II) comprising  
 CC (I); (3) a synthetic or binding molecule (III) comprising a binding site  
 CC identifiable or obtainable by using (I); and (4) determining (M2) a  
 CC minimally essential motif for a binding site, by generating a library of  
 CC test molecules, determining the binding activity of a binding molecule  
 CC with the test molecules, calculating the average binding activity of test  
 CC molecules present in the library comprising a certain motif, and  
 CC determining a motif with a high average binding activity of test  
 CC molecules comprising the motif. (M1) is useful for producing a molecular  
 CC library for identifying or detecting a binding site of TNFalpha. (I) is  
 CC useful for screening for a binding site of TNFalpha capable of  
 CC interacting with a binding molecule, by screening a library with at least  
 CC one potential binding molecule and detecting binding between a member of  
 CC the library and the potential binding molecule. The binding molecule  
 CC comprises a hTNFalpha-2 receptor, and the binding site is a discontinuous  
 CC binding site. (I) and (II) are useful for identifying or obtaining a  
 CC synthetic molecule comprising a binding site of hTNFalpha, or a binding  
 CC molecule capable of binding to a binding site of hTNFalpha. (III) is  
 CC useful for interfering with or effecting binding to a binding molecule of  
 CC hTNFalpha. The molecular libraries produced by (M1) are useful for  
 CC detecting or screening for discontinuous binding sites, in particular in  
 CC relation to binding molecule-ligand interactions such as for e.g. protein  
 CC -protein, protein-nucleic acid and nucleic acid-nucleic acid  
 CC interactions. The identified peptide constructs are useful to develop new  
 CC ligands with agonistic or antagonistic activity for human TNFalpha  
 CC receptor action and are useful in control and prevention of an array of  
 CC diseases with (chronic) inflammatory components such as Crohn's disease  
 CC and other intestinal ulcerations or irritations. The present sequence  
 CC represents a TNFalpha receptor binding peptide which is used in the  
 CC exemplification of the present invention.

XX Sequence 16 AA;

Query Match 100.0%; Score 24; DB 6; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRR 5  
 |||||  
 DB 8 LNRRR 12

RESULT 10

ADAI9851

XX ADAI9851 standard; peptide; 16 AA.

XX ADAI9851;

XX 20-NOV-2003 (first entry)

XX TNFalpha receptor binding peptide SEQ ID NO:25.

XX molecular library; identification; detection; binding site;  
 KW tumour necrosis factor alpha; TNFalpha; protein-protein interaction;  
 KW protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;  
 KW TNFalpha receptor; tumour necrosis factor alpha receptor;  
 KW inflammatory disease; Crohn's disease; intestinal ulceration;  
 KW intestinal irritation.

OS Synthetic.

XX EP1279962-A1.

XX 29-JAN-2003.

XX 27-JUL-2001; 2001EP-00202879.

XX 27-JUL-2001; 2001EP-00202879.

XX (PEPS-) PEPSCAN SYSTEMS BV.

XX Slootstra JW, Puijk WC, Van Dijk E;

XX WPI; 2003-259178/26.

XX Producing molecular library for identifying binding site of tumor  
 PT necrosis factor-alpha, comprises providing the library with many  
 PT molecules produced by segmental linkage of nucleic acids or peptides.

XX Disclosure; Page 20; 70pp; English.

XX The present invention describes a method (M1) for producing a molecular  
 CC library for identifying or detecting a binding site of tumour necrosis  
 CC factor alpha (TNFalpha). (M1) comprises providing the library with  
 CC several molecules, and further generating at least one of the molecules  
 CC by linking a first segment to a second segment. Also described: (1) a  
 CC library (I) comprising several molecules comprising at least a first and  
 CC a second segment obtainable by (M1); (2) a solid support (II) comprising  
 CC (I); (3) a synthetic or binding molecule (III) comprising a binding site  
 CC identifiable or obtainable by using (I); and (4) determining (M2) a  
 CC minimally essential motif for a binding site, by generating a library of  
 CC test molecules, determining the binding activity of a binding molecule  
 CC with the test molecules, calculating the average binding activity of test  
 CC molecules present in the library comprising a certain motif, and  
 CC determining a motif with a high average binding activity of test  
 CC molecules comprising the motif. (M1) is useful for producing a molecular  
 CC library for identifying or detecting a binding site of TNFalpha. (I) is  
 CC useful for screening for a binding site of TNFalpha capable of  
 CC interacting with a binding molecule, by screening a library with at least  
 CC one potential binding molecule and detecting binding between a member of  
 CC the library and the potential binding molecule. The binding molecule  
 CC comprises a hTNFalpha-2 receptor, and the binding site is a discontinuous  
 CC binding site. (I) and (II) are useful for identifying or obtaining a  
 CC synthetic molecule comprising a binding site of hTNFalpha, or a binding  
 CC molecule capable of binding to a binding site of hTNFalpha. (III) is  
 CC useful for interfering with or effecting binding to a binding molecule of  
 CC hTNFalpha. The molecular libraries produced by (M1) are useful for  
 CC detecting or screening for discontinuous binding sites, in particular in  
 CC relation to binding molecule-ligand interactions such as for e.g. protein  
 CC -protein, protein-nucleic acid and nucleic acid-nucleic acid  
 CC interactions. The identified peptide constructs are useful to develop new  
 CC ligands with agonistic or antagonistic activity for human TNFalpha  
 CC receptor action and are useful in control and prevention of an array of  
 CC diseases with (chronic) inflammatory components such as Crohn's disease  
 CC and other intestinal ulcerations or irritations. The present sequence

CC represents a TNFalpha receptor binding peptide which is used in the  
 CC exemplification of the present invention.

SQ Sequence 16 AA;

Query Match 100.0%; Score 24; DB 6; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
 |||||  
 Db 2 LNRRRA 6

RESULT 11

ADA19833  
 ID ADA19833 standard; peptide; 16 AA.

XX AC ADA19833;

XX DT 20-NOV-2003 (first entry)

XX DE TNFalpha receptor binding peptide SEQ ID NO:7.

XX molecular library; identification; detection; binding site;  
 KW tumour necrosis factor alpha; TNFalpha; protein-protein interaction;  
 KW protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;  
 KW TNFalpha receptor; tumour necrosis factor alpha receptor;  
 KW inflammatory disease; Crohn's disease; intestinal ulceration;  
 KW intestinal irritation.

XX OS Synthetic.

XX PN EP1279962-A1.

XX PD 29-JAN-2003.

XX PF 27-JUL-2001; 2001EP-00202879.

XX PR 27-JUL-2001; 2001EP-00202879.

XX PA (PEPS-) PEPSCAN SYSTEMS BV.

XX PI Slootstra JW, Puijk WC, Van Dijk E;

XX DR WPI; 2003-259178/26.

XX PT Producing molecular library for identifying binding site of tumor  
 PT necrosis factor-alpha, comprises providing the library with many  
 PT molecules produced by segmental linkage of nucleic acids or peptides.

XX PS Disclosure; Page 15; 70pp; English.

XX The present invention describes a method (M1) for producing a molecular  
 CC library for identifying or detecting a binding site of tumour necrosis  
 CC factor alpha (TNFalpha). (M1) comprises providing the library with  
 CC several molecules, and further generating at least one of the molecules  
 CC by linking a first segment to a second segment. Also described: (1) a  
 CC library (I) comprising several molecules comprising at least a first and  
 CC a second segment obtainable by (M1); (2) a solid support (II) comprising  
 CC (1); (3) a synthetic or binding molecule (III) comprising a binding site  
 CC identifiable or obtainable by using (1); and (4) determining (M2) a  
 CC minimally essential motif for a binding site, by generating a library of  
 CC test molecules, determining the binding activity of a binding molecule  
 CC with the test molecules, calculating the average binding activity of test  
 CC molecules present in the library comprising a certain motif, and  
 CC determining a motif with a high average binding activity of test  
 CC molecules comprising the motif. (M1) is useful for producing a molecular  
 CC library for identifying or detecting a binding site of TNFalpha. (I) is  
 CC useful for screening for a binding site of TNFalpha capable of  
 CC interacting with a binding molecule, by screening a library with at least  
 CC one potential binding molecule and detecting binding between a member of  
 CC the library and the potential binding molecule. The binding molecule

CC comprises a hTNFalpha-2 receptor, and the binding site is a discontinuous  
 CC binding site. (I) and (II) are useful for identifying or obtaining a  
 CC synthetic molecule comprising a binding site of hTNFalpha, or a binding  
 CC molecule capable of binding to a binding site of hTNFalpha. (III) is  
 CC useful for interfering with or effecting binding to a binding molecule of  
 CC hTNFalpha. The molecular libraries produced by (M1) are useful for  
 CC detecting or screening for discontinuous binding sites, in particular in  
 CC relation to binding molecule-ligand interactions such as for e.g. protein  
 CC -protein, protein-nucleic acid and nucleic acid-nucleic acid  
 CC interactions. The identified peptide constructs are useful to develop new  
 CC ligands with agonistic or antagonistic activity for human TNFalpha  
 CC receptor action and are useful in control and prevention of an array of  
 CC diseases with (chronic) inflammatory components such as Crohn's disease  
 CC and other intestinal ulcerations or irritations. The present sequence  
 CC represents a TNFalpha receptor binding peptide which is used in the  
 CC exemplification of the present invention.

SQ Sequence 16 AA;

Query Match 100.0%; Score 24; DB 6; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
 |||||

Db 1 LNRRRA 5

RESULT 12

ADA19836  
 ID ADA19836 standard; peptide; 16 AA.

XX AC ADA19836;

XX DT 20-NOV-2003 (first entry)

XX DE TNFalpha receptor binding peptide SEQ ID NO:10.

XX molecular library; identification; detection; binding site;  
 KW tumour necrosis factor alpha; TNFalpha; protein-protein interaction;  
 KW protein-nucleic acid interaction; nucleic acid-nucleic acid interaction;  
 KW TNFalpha receptor; tumour necrosis factor alpha receptor;  
 KW inflammatory disease; Crohn's disease; intestinal ulceration;  
 KW intestinal irritation.

XX OS Synthetic.

XX PN EP1279962-A1.

XX PD 29-JAN-2003.

XX PF 27-JUL-2001; 2001EP-00202879.

XX PR 27-JUL-2001; 2001EP-00202879.

XX PA (PEPS-) PEPSCAN SYSTEMS BV.

XX PI Slootstra JW, Puijk WC, Van Dijk E;

XX DR WPI; 2003-259178/26.

XX Producing molecular library for identifying binding site of tumor  
 PT necrosis factor-alpha, comprises providing the library with many  
 PT molecules produced by segmental linkage of nucleic acids or peptides.

XX PS Disclosure; Page 16; 70pp; English.

XX The present invention describes a method (M1) for producing a molecular  
 CC library for identifying or detecting a binding site of tumour necrosis  
 CC factor alpha (TNFalpha). (M1) comprises providing the library with  
 CC several molecules, and further generating at least one of the molecules  
 CC by linking a first segment to a second segment. Also described: (1) a  
 CC library (I) comprising several molecules comprising at least a first and







CC alpha amino acids; V= one of the following dodecapeptide chains:  
CC qwnrranalla, rwdseyanalla, qwisgranalla, lwrantdralf, lwrantdralf, lwrantdralf, or a partial sequence of 5-11 amino acids  
CC from one of the chains, or a peptide chain of 1-4 natural alpha amino acids; M and Q= H, isopropyl, sec-butyl, phenyl, 1-hydroxyethyl, 3-indolyl, 4-imidazolyl-methyl or (CH2)bt; b=1-6; T= OH, MeO, MeS.  
CC isopropyl, phenyl (opt. 4-OH, substd), mercapto, amino, carboxy, carbamoyl or guanidino; or M and Q together are (CH2)c-S-S-(CH2)d, (CH2)eCO NH-(CH2)f or (CH2)2eNH CO(CH2)gNH CO(CH2)h; c and d=1-4; e and f=1-6; g=1-12. The peptide is a low mol. wt. deriv. of TNF. See also DE3841753-55, DE3841759, DE3841761-64, DE3841767-68. (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 20 AA;  
Query Match 100.0%; Score 24; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LNRRRA 5  
Db 14 LNRRRA 18  
|||||  
RESULT 15  
AAR06807  
ID AAR06807 standard; protein; 21 AA.  
XX  
AC AAR06807;  
XX  
DT 25-MAR-2003 (revised)  
DT 24-OCT-1990 (first entry)  
XX  
DE Tumour necrosis factor derived peptide.  
XX  
XX Tumour necrosis factor; TNF; neoplastic disease; autoimmune disease; infection; inflammation; transplant rejection; cyclic.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 21..21 /label= OTHER  
FT FT /note= "Ahx"  
XX  
PN DE3841767-A.  
XX  
PD 13-JUN-1990.  
XX  
XX 12-DEC-1988; 88DE-03841767.  
XX  
PR 12-DEC-1988; 88DE-03841767.  
XX  
XX (BADI ) BASP AG.  
PA (BOEH/) BOEHM H J.  
XX  
PI Bohm HJ, Daum L, Haupt A, Schmied B, Walker N, Zechel JC;  
XX  
DR WFI; 1990-186583/25.  
XX  
XX Peptide tumour necrosis factor analogues - used in treatment of tumours and auto-immune diseases.  
XX  
XX  
XX Example 59; Page 13; 16pp; German.  
XX  
CC This peptide is an example of a highly generic sequence of the formula X-A-B-E-Leu-Y A= Glu, Pro or Gln; B= Gly, Glu, Asn or Asp; E= Gln or Ser; X= G-NH-CHM-CO-W, G-NH-CHM-CO or G-R-NH-CHM-CO-W; Y= Z, NH-CHQ-CO-Z, V-NH-CHQ-CO-Z, NH-CHQ-CO-U-Z or V-NH-CHQ-CO-U-Z; G= H or a protecting group; Z= OH, NH2 or carboxy protecting group; or G and Z together are a covalent bond or the gp. CO(CH2)2NH; a=1-12; R and U= peptide chains of 1-5 naturally occurring alpha amino acids; W= one of the following dodecapeptide chains: kpahvvpqga, kpahvvpqga, kpahvvpqgv,

CC kpahvvpqgv, kpahhlgdpok, kpahhlgdpst, kpahhlgvypsk, or a partial sequence of 5-11 amino acids from one of the chains, or a peptide chain of 1-4 naturally occurring alpha amino acids; V= one of the following dodecapeptide chains: qwnrranalla, rwdseyanalla, qwisgranalla, lwrantdralf, lwrantdralf, lwrantdralf, lwrantdralf, lwrantdralf, or a partial sequence of 5-11 amino acids from one of the chains, or a peptide chain of 1-4 natural alpha amino acids; M and Q= H, isopropyl, sec-butyl, phenyl, 1-hydroxyethyl, 3-indolyl, 4-imidazolyl-methyl or (CH2)bt; b=1-6; T= OH, MeO, MeS, isopropyl, phenyl (opt. 4-OH, substd), mercapto, amino, carboxy, carbamoyl or guanidino; or M and Q together are (CH2)c-S-S-(CH2)d, (CH2)eCO NH-(CH2)f or (CH2)2eNH CO(CH2)gNH CO(CH2)h; c and d=1-4; e and f=1-6; g=1-12. The peptide is a low mol. wt. deriv. of TNF. See also DE3841753-55, DE3841759, DE3841761-64, DE3841767-68. (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 21 AA;  
Query Match 100.0%; Score 24; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LNRRRA 5  
Db 14 LNRRRA 18  
|||||  
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Job time : 72.5 secs

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OM protein - protein search, using sw model

Run on: January 12, 2006, 16:12:40 ; Search time 19 Seconds  
(without alignments)  
21.757 Million cell updates/sec

Title: US-10-716-030-1

Perfect score: 24

Sequence: 1 LNRA 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PTCUS\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	19	1	US-08-107-235-9
2	24	100.0	19	1	US-08-178-268-43
3	24	100.0	19	2	US-08-714-960B-9
4	24	100.0	19	2	US-09-598-784-9
5	24	100.0	51	2	US-09-369-494-16
6	24	100.0	51	2	US-09-358-569D-14
7	24	100.0	51	2	US-09-569-670-16
8	24	100.0	69	2	US-09-513-999C-5811
9	24	100.0	71	2	US-09-632-287A-20
10	24	100.0	71	2	US-10-286-696-20
11	24	100.0	99	2	US-09-314-268-133
12	24	100.0	104	2	US-09-911-777-5
13	24	100.0	139	1	US-07-994-469A-10
14	24	100.0	145	1	US-07-994-469A-9
15	24	100.0	147	1	US-07-668-517-1
16	24	100.0	147	2	US-09-105-343A-9
17	24	100.0	147	2	US-09-565-423-4
18	24	100.0	148	1	US-07-668-517-2
19	24	100.0	148	1	US-07-668-517-15
20	24	100.0	149	1	US-07-668-517-3
21	24	100.0	149	1	US-07-668-517-16
22	24	100.0	150	1	US-07-668-517-4
23	24	100.0	150	1	US-07-668-517-5
24	24	100.0	150	1	US-07-668-517-6
25	24	100.0	150	1	US-07-668-517-8
26	24	100.0	150	1	US-07-668-517-9
27	24	100.0	150	1	US-07-668-517-10

28	24	100.0	150	1	US-07-668-517-11
29	24	100.0	150	1	US-07-668-517-12
30	24	100.0	150	1	US-07-668-517-13
31	24	100.0	150	1	US-07-668-517-14
32	24	100.0	150	1	US-07-668-517-17
33	24	100.0	150	1	US-07-668-517-29
34	24	100.0	150	1	US-07-668-517-31
35	24	100.0	150	1	US-07-668-517-35
36	24	100.0	150	1	US-07-668-517-37
37	24	100.0	150	1	US-07-994-469A-6
38	24	100.0	150	1	US-07-994-469A-7
39	24	100.0	150	1	US-07-994-469A-8
40	24	100.0	150	1	US-07-994-469A-57
41	24	100.0	150	2	US-09-286-529-25
42	24	100.0	151	1	US-07-668-517-7
43	24	100.0	151	1	US-07-668-517-18
44	24	100.0	151	1	US-07-668-517-19
45	24	100.0	151	1	US-07-668-517-20

ALIGNMENTS

RESULT 1  
US-08-107-235-9  
; Sequence 9, Application US/08107235  
; Patent No. 5587457  
; GENERAL INFORMATION:  
; APPLICANT: Rathjen, Deborah A  
; APPLICANT: Ferrante, Antonio  
; APPLICANT: Widmer, Fred  
; TITLE OF INVENTION: Neutrophil Stimulating Peptides  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Allegretti & Witcoff, Ltd.  
; STREET: 10 S. Wacker Dr.  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/107,235  
; FILING DATE: 16-AUG-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/930,415  
; FILING DATE: 12-MAR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McDonnell, John J  
; REGISTRATION NUMBER: 26,949  
; REFERENCE/DOCKET NUMBER: 92,622A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-715-1000  
; TELEFAX: 312-715-1234  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..19  
; OTHER INFORMATION: /note= "PEPTIDE 307 (22-40)"  
US-08-107-235-9  
Query Match 100.0%; Score 24; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 24;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRR 5  
Db 8 LNRR 12

## RESULT 2

US-08-178-268-43  
; Sequence 43, Application US/08178268  
; Patent No. 5795859  
; GENERAL INFORMATION:  
; APPLICANT: RATHJEN, Deborah A  
; APPLICANT: WIDMER, Fred  
; APPLICANT: GRIGG, Geoffrey W  
; APPLICANT: MACK, Philip O  
; TITLE OF INVENTION: Peptide which Abrogates TNF and/or LPS Toxicity  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon & Vanderhye P.C.  
; STREET: 1100 No. 5795859th Glebe Road, 8th Floor  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/178,268  
; FILING DATE: 05-JAN-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MITCHARD, Leonard C  
; REGISTRATION NUMBER: 29,009  
; REFERENCE/DOCKET NUMBER: 47-45  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; TELEFAX: (703) 816-4100  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: both  
; MOLECULE TYPE: peptide  
US-08-178-268-43

Query Match 100.0%; Score 24; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRR 5  
Db 8 LNRR 12

## RESULT 3

US-08-714-960B-9  
; Sequence 9, Application US/08714960B  
; Patent No. 6121237  
; GENERAL INFORMATION:  
; APPLICANT: RATHJEN, Deborah A  
; APPLICANT: FERRANTE, Antonio  
; TITLE OF INVENTION: Neutrophil Stimulating Peptides  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER & WITCOFF, LTD.  
; STREET: 10 S. Wacker Drive, Suite 3000  
; CITY: Chicago  
; STATE: Illinois

; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: IBM compatible PC/MS-DOS  
; SOFTWARE: WordPerfect version 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/714,960B  
; FILING DATE: 17-SEP-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU PJ9065  
; FILING DATE: 12-MAR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/AU91/00086  
; FILING DATE: 12-MAR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/930,415  
; FILING DATE: 09-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/107,235  
; FILING DATE: 16-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Resie, Robert H.  
; REGISTRATION NUMBER: 32,168  
; REFERENCE/DOCKET NUMBER: 92,622-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 715-1000  
; TELEFAX: (312) 715-1234  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..19  
; OTHER INFORMATION: /note= "PEPTIDE 307 (22-40) "  
US-08-714-960B-9

Query Match 100.0%; Score 24; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRR 5  
Db 8 LNRR 12

## RESULT 4

US-09-598-784-9  
; Sequence 9, Application US/09598784  
; Patent No. 6375928  
; GENERAL INFORMATION:  
; APPLICANT: RATHJEN, Deborah A  
; FERRANTE, Antonio  
; TITLE OF INVENTION: Neutrophil Stimulating Peptides  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER & WITCOFF, LTD.  
; STREET: 10 S. Wacker Drive, Suite 3000  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: IBM compatible PC/MS-DOS  
; SOFTWARE: WordPerfect version 6.1

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 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/598,784  
 ; FILING DATE: 21-Jun-2000  
 ; CLASSIFICATION: <Unknown>  
 ;  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: AU PJ9065  
 ; FILING DATE: 12-MAR-1990  
 ; APPLICATION NUMBER: PCT/AU91/00086  
 ; FILING DATE: 12-MAR-1991  
 ; APPLICATION NUMBER: US 07/930,415  
 ; FILING DATE: 09-NOV-1992  
 ; APPLICATION NUMBER: US 08/107,235  
 ; FILING DATE: 16-AUG-1993  
 ; APPLICATION NUMBER: US 08/714,960  
 ; FILING DATE: 17-SEP-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Resis, Robert H.  
 ; REGISTRATION NUMBER: 32,168  
 ; REFERENCE/DOCKET NUMBER: 11341.00001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (312) 715-1000  
 ; TELEFAX: (312) 715-1234  
 ; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 19 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: not relevant  
 ; MOLECULE TYPE: peptide  
 ; FEATURE:  
 ; NAME/KEY: Peptide  
 ; LOCATION: 1..19  
 ; OTHER INFORMATION: /note= "PEPTIDE 307 (22-40)"  
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 ; SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
 ;  
 ; US-09-598-784-9

Query Match 100.0%; Score 24; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
 DB 8 LNRRRA 12

RESULT 5  
 US-09-369-494-16  
 ; Sequence 16, Application US/09369494  
 ; Patent No. 6180607  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Davies, Christopher  
 ; APPLICANT: Chen, Dadong  
 ; APPLICANT: Rocznik, Steve  
 ; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity  
 ; FILE REFERENCE: MSB-7260  
 ; CURRENT APPLICATION NUMBER: US/09/369,494  
 ; CURRENT FILING DATE: 1999-08-05  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 16  
 ; LENGTH: 51  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:fragment from  
 ; OTHER INFORMATION: computer database  
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 ; US-09-369-494-16

Query Match 100.0%; Score 24; DB 2; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 66;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5

DB 19 LNRRRA 23

RESULT 6  
 US-09-358-569D-14  
 ; Sequence 14, Application US/09358569D  
 ; Patent No. 6294648  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Delaria, Kathy  
 ; APPLICANT: Rocznik, Steve  
 ; APPLICANT: Davies, Christopher  
 ; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity  
 ; FILE REFERENCE: MSB-7259  
 ; CURRENT APPLICATION NUMBER: US/09/358,569D  
 ; CURRENT FILING DATE: 1999-07-20  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 14  
 ; LENGTH: 51  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:from computer  
 ; OTHER INFORMATION: database  
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 ; US-09-358-569D-14

Query Match 100.0%; Score 24; DB 2; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 66;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
 DB 19 LNRRRA 23

RESULT 7  
 US-09-569-670-16  
 ; Sequence 16, Application US/09569670  
 ; Patent No. 6689582  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Davies, Christopher  
 ; APPLICANT: Chen, Dadong  
 ; APPLICANT: Rocznik, Steve  
 ; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity  
 ; FILE REFERENCE: MSB-7260  
 ; CURRENT APPLICATION NUMBER: US/09/569,670  
 ; CURRENT FILING DATE: 2000-05-12  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 16  
 ; LENGTH: 51  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:fragment from  
 ; OTHER INFORMATION: computer database  
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 ; US-09-569-670-16

Query Match 100.0%; Score 24; DB 2; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 66;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
 DB 19 LNRRRA 23

RESULT 8  
 US-09-513-999C-5811  
 ; Sequence 5811, Application US/09513999C  
 ; Patent No. 6783961  
 ; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 5811  
; LENGTH: 69  
; TYPE: PRT  
; ORGANISM: Homo sapiens

; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 48  
; OTHER INFORMATION: Xaa= \* or Leu or Ser or Trp  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 56  
; OTHER INFORMATION: Xaa=Ser or Thr  
US-09-513-999C-5811

Query Match 100.0%; Score 24; DB 2; Length 69;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRRA 5  
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Db 35 LNRRRA 39

## RESULT 9

US-09-632-287A-20  
; Sequence 20, Application US/09632287A  
; Patent No. 6521422  
; GENERAL INFORMATION:

; APPLICANT: Hsu, Hailing  
; APPLICANT: Wooden, Scott K  
; APPLICANT: Boyle, William J  
; TITLE OF INVENTION: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family  
; FILE REFERENCE: 01017/35550A

; CURRENT APPLICATION NUMBER: US/09/632,287A  
; CURRENT FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: US 60/147,294  
; PRIOR FILING DATE: 1999-08-04  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 71  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-632-287A-20

Query Match 100.0%; Score 24; DB 2; Length 71;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRRA 5  
|||||  
Db 24 LNRRRA 28

## RESULT 10

US-10-286-696-20  
; Sequence 20, Application US/10286696  
; Patent No. 6852839  
; GENERAL INFORMATION:  
; APPLICANT: Hsu, Hailing  
; APPLICANT: Wooden, Scott K

; APPLICANT: Boyle, William J  
; TITLE OF INVENTION: Fhm, A No. 6852839el Member of the TNF Ligand Supergene Family  
; FILE REFERENCE: 01017/35550A  
; CURRENT APPLICATION NUMBER: US/10/286,696  
; CURRENT FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: US 60/147,294  
; PRIOR FILING DATE: 1999-08-04  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 71  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-286-696-20

Query Match 100.0%; Score 24; DB 2; Length 71;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRRA 5  
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Db 24 LNRRRA 28

## RESULT 11

US-09-314-268-133  
; Sequence 133, Application US/09314268  
; Patent No. 6346377  
; GENERAL INFORMATION:

; APPLICANT: Doobar, John  
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR PAPILLOMA  
; FILE REFERENCE: 3789/80902  
; CURRENT APPLICATION NUMBER: US/09/314,268  
; CURRENT FILING DATE: 1999-03-19  
; EARLIER APPLICATION NUMBER: 09/314,268  
; EARLIER FILING DATE: 1999-05-18  
; NUMBER OF SEQ ID NOS: 179  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 133  
; LENGTH: 99  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 20

US-09-314-268-133

Query Match 100.0%; Score 24; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRRA 5  
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Db 46 LNRRRA 50

## RESULT 12

US-09-911-777-5  
; Sequence 5, Application US/09911777  
; Patent No. 6869605  
; GENERAL INFORMATION:

; APPLICANT: BIOGEN, INC.  
; APPLICANT: APOTEC S.A.  
; APPLICANT: BROWNING, Jeffrey  
; APPLICANT: AMBROSE, Christine  
; APPLICANT: MACKAY, Fabienne  
; APPLICANT: TSCHOPP, Jurg  
; APPLICANT: SCHNEIDER, Pascal  
; TITLE OF INVENTION: BAFF, Inhibitors Thereof and Their Use  
; FILE REFERENCE: A070 US  
; CURRENT APPLICATION NUMBER: US/09/911,777  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/117,169  
; PRIOR FILING DATE: 1999-01-25

;; PRIOR APPLICATION NUMBER: 60/143,228  
;; PRIOR FILING DATE: 1999-07-09  
;; PRIOR APPLICATION NUMBER: PCT/US00/01788  
;; PRIOR FILING DATE: 2000-01-25  
;; NUMBER OF SEQ ID NOS: 22  
;; SOFTWARE: FASTSEQ for Windows Version 4.0  
;; SEQ ID NO 5  
;; TYPE: PRT  
;; LENGTH: 104  
;; ORGANISM: Homo Sapien  
US-09-911-777-5

Query Match 100.0%; Score 24; DB 2; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRA 5  
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DB 21 LNRA 25

RESULT 13  
US-07-994-469A-10  
; Sequence 10, Application US/07994469A  
; Patent No. 5519119  
; GENERAL INFORMATION:  
; APPLICANT: Yamada, No. 5519119utoshio  
; APPLICANT: Kato, Masanari  
; APPLICANT: Miyata, Keizo  
; APPLICANT: Aoyama, Yoshiyuki  
; APPLICANT: Shikama, Hiroshi  
; TITLE OF INVENTION: Polypeptide  
; NUMBER OF SEQUENCES: 101  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 Jefferson Davis Highway, Fourth Floor  
; CITY: Arlington  
; STATE: Virginia  
; ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/994,469A  
FILING DATE: 21-DEC-1992

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Oblon, No. 5519119man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 72-085-0 FWC  
TELEPHONE: (703)413-3000  
TELEFAX: (703)413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 139 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-994-469A-10

Query Match 100.0%; Score 24; DB 1; Length 139;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRA 5  
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DB 19 LNRA 23

RESULT 14  
US-07-994-469A-9  
; Sequence 9, Application US/07994469A  
; Patent No. 5519119  
; GENERAL INFORMATION:  
; APPLICANT: Yamada, No. 5519119utoshio  
; APPLICANT: Kato, Masanari  
; APPLICANT: Miyata, Keizo  
; APPLICANT: Aoyama, Yoshiyuki  
; APPLICANT: Shikama, Hiroshi  
; TITLE OF INVENTION: Polypeptide  
; NUMBER OF SEQUENCES: 101  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 Jefferson Davis Highway, Fourth Floor  
; CITY: Arlington  
; STATE: Virginia  
; ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/994,469A  
FILING DATE: 21-DEC-1992

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Oblon, No. 5519119man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 72-085-0 FWC  
TELEPHONE: (703)413-3000  
TELEFAX: (703)413-2220

TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 145 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-994-469A-9

Query Match 100.0%; Score 24; DB 1; Length 145;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRA 5  
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DB 25 LNRA 29

RESULT 15  
US-07-668-517-1  
; Sequence 1, Application US/07668517  
; Patent No. 5262309  
; GENERAL INFORMATION:  
; APPLICANT: SATOSHI NAKAMURA et al.  
; TITLE OF INVENTION: No. 5262309el Physiologically Active  
; TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism  
; TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb



; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/668,517  
; FILING DATE: 19910322  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Matthew Jacob  
; REGISTRATION NUMBER: 25,154  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX: 202-371-8856  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 147 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
US-07-668-517-1

Query Match 100.0%; Score 24; DB 1; Length 147;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LNRRR 5  
Db 19 LNRRR 23

Search completed: January 12, 2006, 16:20:05  
Job time : 19 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 12, 2006, 16:19:26 ; Search time 15.5 Seconds  
(without alignments)  
3.050 Million cell updates/sec

Title: US-10-716-030-1  
Perfect score: 24  
Sequence: 1 LNRRRA 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New.\*  
1: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
5: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
6: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
7: /cgn2\_6/prodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match	Length	ID	Description
1	24	100.0	102	6	US-10-689-742-21	Sequence 21, Appl
2	24	100.0	104	7	US-11-065-669-5	Sequence 5, Appl1
3	24	100.0	157	7	US-11-010-954-1	Sequence 1, Appl1
4	24	100.0	157	7	US-11-053-750-1	Sequence 1, Appl1
5	24	100.0	157	7	US-11-053-749-1	Sequence 1, Appl1
6	24	100.0	157	7	US-11-108-001-12	Sequence 12, Appl
7	24	100.0	158	7	US-11-082-544-4	Sequence 4, Appl1
8	24	100.0	164	7	US-11-108-001-2	Sequence 2, Appl1
9	24	100.0	180	7	US-11-082-544-8	Sequence 8, Appl1
10	24	100.0	399	7	US-11-065-943-53	Sequence 53, Appl
11	24	100.0	401	7	US-11-055-822-336	Sequence 336, App
12	24	100.0	421	7	US-11-120-308-64	Sequence 64, Appl
13	24	100.0	440	7	US-11-102-240-134	Sequence 134, App
14	22	91.7	164	6	US-10-467-657-9140	Sequence 9140, Ap
15	22	91.7	229	6	US-10-467-657-916	Sequence 916, App
16	22	91.7	378	6	US-10-467-657-1796	Sequence 1796, Ap
17	22	91.7	547	7	US-11-156-003-16	Sequence 16, Appl
18	22	91.7	1827	7	US-11-057-058-62	Sequence 62, Appl
19	21	87.5	295	6	US-10-467-657-620	Sequence 620, App
20	21	87.5	311	6	US-10-873-528-117	Sequence 117, App
21	21	87.5	322	6	US-10-689-742-46	Sequence 46, Appl
22	21	87.5	322	6	US-10-821-234-891	Sequence 891, App
23	21	87.5	347	6	US-10-821-234-1379	Sequence 1379, Ap
24	21	87.5	350	6	US-10-467-657-1972	Sequence 1972, Ap
25	21	87.5	409	7	US-11-113-424-73	Sequence 73, Appl

26	21	87.5	449	6	US-10-763-712A-83	Sequence 83, Appl
27	21	87.5	478	6	US-10-793-626-1348	Sequence 1348, Ap
28	21	87.5	503	7	US-11-113-424-72	Sequence 72, Appl
29	21	87.5	559	6	US-10-821-234-1513	Sequence 1513, Ap
30	21	87.5	570	7	US-11-113-424-69	Sequence 69, Appl
31	21	87.5	570	7	US-11-113-424-71	Sequence 71, Appl
32	21	87.5	620	7	US-11-113-424-70	Sequence 70, Appl
33	21	87.5	676	6	US-10-510-947-1	Sequence 1, Appl1
34	21	87.5	720	7	US-11-113-424-28	Sequence 28, Appl
35	21	87.5	747	7	US-11-113-424-26	Sequence 26, Appl
36	21	87.5	756	6	US-10-467-657-8694	Sequence 8694, Ap
37	21	87.5	783	7	US-11-082-389-354	Sequence 354, App
38	21	87.5	1368	6	US-10-770-303-2	Sequence 2, Appl1
39	21	87.5	1368	7	US-11-185-372-2	Sequence 2, Appl1
40	20	83.3	53	6	US-10-467-657-6170	Sequence 6170, Ap
41	20	83.3	60	6	US-10-502-972-13	Sequence 13, Appl
42	20	83.3	60	6	US-10-502-972-17	Sequence 17, Appl
43	20	83.3	60	6	US-10-502-972-19	Sequence 19, Appl
44	20	83.3	61	6	US-10-467-657-1222	Sequence 1222, Ap
45	20	83.3	61	6	US-10-467-657-9027	Sequence 9027, Ap

ALIGNMENTS

RESULT 1  
US-10-689-742-21  
; Sequence 21, Application US/10689742  
; Publication No. US20050250180A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M  
; APPLICANT: Lavallic, Edward R  
; APPLICANT: Racie, Lisa A  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Spaulding, Vikki  
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
; FILE REFERENCE: 00766.000091.10  
; CURRENT APPLICATION NUMBER: US/10/689,742  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 09/746,783  
; PRIOR FILING DATE: 2000-12-21  
; NUMBER OF SEQ ID NOS: 231  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 21  
; LENGTH: 102  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-689-742-21

Query Match 100.0%; Score 24; DB 6; Length 102;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
|||  
Db 84 LNRRRA 88

RESULT 2  
US-11-065-669-5  
; Sequence 5, Application US/11065669  
; Publication No. US2005024411A1  
; GENERAL INFORMATION:  
; APPLICANT: MacKay, Fabienne  
; APPLICANT: Kalled, Susan  
; TITLE OF INVENTION: BAPF, INHIBITORS THEREOF AND THEIR USE IN THE  
; TITLE OF INVENTION: MODULATION OF B-CELL RESPONSE  
; FILE REFERENCE: 08201.0024-0400  
; CURRENT APPLICATION NUMBER: US/11/065,669  
; CURRENT FILING DATE: 2005-02-24

;; PRIOR APPLICATION NUMBER: 10/045,574  
;; PRIOR FILING DATE: 2001-11-07  
;; PRIOR APPLICATION NUMBER: 09/911,777  
;; PRIOR FILING DATE: 2001-07-24  
;; PRIOR APPLICATION NUMBER: 60/143,228  
;; PRIOR FILING DATE: 2001-07-09  
;; PRIOR APPLICATION NUMBER: PCT/US00/01788  
;; PRIOR FILING DATE: 2000-01-25  
;; PRIOR APPLICATION NUMBER: 60/117,169  
;; PRIOR FILING DATE: 1999-01-25  
;; NUMBER OF SEQ ID NOS: 26  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 5  
;; LENGTH: 104  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-11-065-669-5

Query Match 100.0%; Score 24; DB 7; Length 104;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRRA 5  
|||||  
Db 21 LNRRRA 25

RESULT 3  
US-11-010-954-1  
;; Sequence 1, Application US/11010954  
;; Publication No. US20050249735A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Le, Junming  
;; APPLICANT: Vilcek, Jan  
;; APPLICANT: Daddona, Peter  
;; APPLICANT: Ghayeb, John  
;; APPLICANT: Knight, David  
;; APPLICANT: Siegel, Scott  
;; APPLICANT: Shealy, David  
;; TITLE OF INVENTION: Methods of Treating Ankylosing Spondylitis Using Anti-TNF Antibody  
;; FILE REFERENCE: 0975.1005-043  
;; CURRENT APPLICATION NUMBER: US/11/010,954  
;; CURRENT FILING DATE: 2004-12-13  
;; PRIOR APPLICATION NUMBER: US 10/637,759  
;; PRIOR FILING DATE: 2003-08-08  
;; PRIOR APPLICATION NUMBER: US 09/920,137  
;; PRIOR FILING DATE: 2001-08-01  
;; PRIOR APPLICATION NUMBER: US 09/927,703  
;; PRIOR FILING DATE: 2001-08-10  
;; PRIOR APPLICATION NUMBER: US 09/756,398  
;; PRIOR FILING DATE: 2001-01-08  
;; PRIOR APPLICATION NUMBER: US 60/236,826  
;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: US 60/223,360  
;; PRIOR FILING DATE: 2000-08-07  
;; NUMBER OF SEQ ID NOS: 30  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1  
;; LENGTH: 157  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-11-010-954-1

Query Match 100.0%; Score 24; DB 7; Length 157;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRRA 5  
|||||  
Db 29 LNRRRA 33

RESULT 4  
US-11-053-750-1  
;; Sequence 1, Application US/11053750  
;; Publication No. US20050255104A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Le, Junming  
;; APPLICANT: Vilcek, Jan  
;; APPLICANT: Daddona, Peter  
;; APPLICANT: Ghayeb, John  
;; APPLICANT: Knight, David  
;; APPLICANT: Siegel, Scott  
;; APPLICANT: Scallion, Bernard  
;; TITLE OF INVENTION: Methods of Treating Psoriasis Using  
;; TITLE OF INVENTION: Anti-TNF Receptor Fusion Proteins  
;; FILE REFERENCE: 0975.1005-045  
;; CURRENT APPLICATION NUMBER: US/11/053,750  
;; CURRENT FILING DATE: 2005-02-07  
;; PRIOR APPLICATION NUMBER: U.S. 09/927,703  
;; PRIOR FILING DATE: 2001-08-10  
;; PRIOR APPLICATION NUMBER: U.S. 09/756,398  
;; PRIOR FILING DATE: 2001-01-08  
;; PRIOR APPLICATION NUMBER: U.S. 09/133,119  
;; PRIOR FILING DATE: 1998-08-12  
;; PRIOR APPLICATION NUMBER: U.S. 08/570,674  
;; PRIOR FILING DATE: 1995-12-11  
;; PRIOR APPLICATION NUMBER: U.S. 08/324,799  
;; PRIOR FILING DATE: 1994-10-18  
;; PRIOR APPLICATION NUMBER: U.S. 08/192,102  
;; PRIOR FILING DATE: 1994-02-04  
;; PRIOR APPLICATION NUMBER: U.S. 08/192,861  
;; PRIOR FILING DATE: 1994-02-04  
;; PRIOR APPLICATION NUMBER: U.S. 08/192,093  
;; PRIOR FILING DATE: 1994-02-04  
;; PRIOR APPLICATION NUMBER: U.S. 09/010,406  
;; PRIOR FILING DATE: 1993-01-29  
;; PRIOR APPLICATION NUMBER: U.S. 08/013,413  
;; PRIOR FILING DATE: 1993-02-02  
;; NUMBER OF SEQ ID NOS: 30  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1  
;; LENGTH: 157  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-11-053-750-1

Query Match 100.0%; Score 24; DB 7; Length 157;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRRA 5  
|||||  
Db 29 LNRRRA 33

RESULT 5  
US-11-053-749-1  
;; Sequence 1, Application US/11053749  
;; Publication No. US20050260201A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Le, Junming  
;; APPLICANT: Vilcek, Jan  
;; APPLICANT: Daddona, Peter  
;; APPLICANT: Ghayeb, John  
;; APPLICANT: Knight, David  
;; APPLICANT: Siegel, Scott  
;; APPLICANT: Scallion, Bernard  
;; TITLE OF INVENTION: Methods of Treating Rheumatoid Arthritis  
;; TITLE OF INVENTION: Using Anti-TNF Receptor Fusion Proteins  
;; FILE REFERENCE: 0975.1005-040  
;; CURRENT APPLICATION NUMBER: US/11/053,749  
;; CURRENT FILING DATE: 2005-02-07  
;; PRIOR APPLICATION NUMBER: US/09/927,703  
;; PRIOR FILING DATE: 2001-08-10

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; PRIOR APPLICATION NUMBER: U.S. 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-053-749-1

Query Match      100.0%; Score 24; DB 7; Length 157;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNRA 5
        |||||
Db      29 LNRA 33

RESULT 6
US-11-108-001-12
; Sequence 12, Application US/11108001
; Publication No. US20050265962A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Steed, Paul Michael
; APPLICANT: Zalevsky, Jonathan
; APPLICANT: Szymkowski, David Edmund
; TITLE OF INVENTION: PROTEIN BASED TNF-ALPHA VARIANTS FOR THE TREATMENT OF TNF-ALPHA
; TITLE OF INVENTION: RELATED DISORDERS
; FILE REFERENCE: A-68990-7
; CURRENT APPLICATION NUMBER: US/11/108,001
; CURRENT FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US 10/963,994
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 09/798,789
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 09/945,150
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 09/981,289
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 10/262,630
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US 60/553,908
; PRIOR FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: US 60/510,430
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/509,960
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/528,275
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: US 60/523,647
; PRIOR FILING DATE: 2003-11-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 12
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-108-001-12

Query Match      100.0%; Score 24; DB 7; Length 157;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNRA 5
        |||||
Db      29 LNRA 33

RESULT 7
US-11-082-544-4
; Sequence 4, Application US/11082544
; Publication No. US20050249706A1
; GENERAL INFORMATION:
; APPLICANT: Bermudes, G.
; APPLICANT: King, I.
; APPLICANT: Clairmont, C.
; APPLICANT: Lin, S.
; APPLICANT: Belcourt, M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
; FILE REFERENCE: 8002-059
; CURRENT APPLICATION NUMBER: US/11/082,544
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US/09/645,415
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/157,581
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 60/157,637
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-082-544-4

Query Match      100.0%; Score 24; DB 7; Length 158;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNRA 5
        |||||
Db      30 LNRA 34

RESULT 8
US-11-108-001-2
; Sequence 2, Application US/11108001
; Publication No. US20050265962A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Steed, Paul Michael
; APPLICANT: Zalevsky, Jonathan
; APPLICANT: Szymkowski, David Edmund
; TITLE OF INVENTION: PROTEIN BASED TNF-ALPHA VARIANTS FOR THE TREATMENT OF TNF-ALPHA
; TITLE OF INVENTION: RELATED DISORDERS
; FILE REFERENCE: A-68990-7
; CURRENT APPLICATION NUMBER: US/11/108,001
; CURRENT FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US 10/963,994
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 09/798,789
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 09/945,150
; PRIOR FILING DATE: 2001-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
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; SEQ ID NO 12
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-108-001-12

Query Match      100.0%; Score 24; DB 7; Length 157;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNRA 5
        |||||
Db      29 LNRA 33

RESULT 7
US-11-082-544-4
; Sequence 4, Application US/11082544
; Publication No. US20050249706A1
; GENERAL INFORMATION:
; APPLICANT: Bermudes, G.
; APPLICANT: King, I.
; APPLICANT: Clairmont, C.
; APPLICANT: Lin, S.
; APPLICANT: Belcourt, M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
; FILE REFERENCE: 8002-059
; CURRENT APPLICATION NUMBER: US/11/082,544
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US/09/645,415
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/157,581
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 60/157,637
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-082-544-4

Query Match      100.0%; Score 24; DB 7; Length 158;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNRA 5
        |||||
Db      30 LNRA 34

RESULT 8
US-11-108-001-2
; Sequence 2, Application US/11108001
; Publication No. US20050265962A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Steed, Paul Michael
; APPLICANT: Zalevsky, Jonathan
; APPLICANT: Szymkowski, David Edmund
; TITLE OF INVENTION: PROTEIN BASED TNF-ALPHA VARIANTS FOR THE TREATMENT OF TNF-ALPHA
; TITLE OF INVENTION: RELATED DISORDERS
; FILE REFERENCE: A-68990-7
; CURRENT APPLICATION NUMBER: US/11/108,001
; CURRENT FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US 10/963,994
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 09/798,789
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 09/945,150
; PRIOR FILING DATE: 2001-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
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;; PRIOR APPLICATION NUMBER: US 09/981,289  
;; PRIOR FILING DATE: 2001-10-15  
;; PRIOR APPLICATION NUMBER: US 10/262,630  
;; PRIOR FILING DATE: 2002-09-30  
;; PRIOR APPLICATION NUMBER: US 60/553,908  
;; PRIOR FILING DATE: 2004-03-17  
;; PRIOR APPLICATION NUMBER: US 60/510,430  
;; PRIOR FILING DATE: 2003-10-10  
;; PRIOR APPLICATION NUMBER: US 60/509,960  
;; PRIOR FILING DATE: 2003-10-09  
;; PRIOR APPLICATION NUMBER: US 60/528,275  
;; PRIOR FILING DATE: 2003-12-08  
;; PRIOR APPLICATION NUMBER: US 60/523,647  
;; PRIOR FILING DATE: 2003-11-20  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 13  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 2  
;; LENGTH: 164  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-11-108-001-2

Query Match 100.0%; Score 24; DB 7; Length 164;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
|||||  
Db 36 LNRRRA 40

RESULT 9  
US-11-082-544-8  
;; Sequence 8, Application US/11082544  
;; Publication No. US20050249706A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Bermudes, G.  
;; APPLICANT: King, I.  
;; APPLICANT: Clairmont, C.  
;; APPLICANT: Lin, S.  
;; APPLICANT: Belcourt, M.  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
;; TITLE OF INVENTION: TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES  
;; FILE REFERENCE: 8002-059  
;; CURRENT APPLICATION NUMBER: US/11/082,544  
;; CURRENT FILING DATE: 2005-03-17  
;; PRIOR APPLICATION NUMBER: US/09/645,415  
;; PRIOR FILING DATE: 2000-08-24  
;; PRIOR APPLICATION NUMBER: 60/157,581  
;; PRIOR FILING DATE: 1999-10-04  
;; PRIOR APPLICATION NUMBER: 60/157,637  
;; PRIOR FILING DATE: 1999-10-04  
;; NUMBER OF SEQ ID NOS: 61  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 8  
;; LENGTH: 180  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Fusion construct  
US-11-082-544-8

Query Match 100.0%; Score 24; DB 7; Length 180;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
|||||  
Db 52 LNRRRA 56

RESULT 10

US-11-065-943-53  
;; Sequence 53, Application US/11065943  
;; Publication No. US20050250131A1  
;; GENERAL INFORMATION:  
;; APPLICANT: JESTIN, JEAN-LUC  
;; APPLICANT: VICHIER-GUERRE, SOPHIE  
;; APPLICANT: FERRIS, STEPHANE  
;; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I  
;; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,  
;; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME  
;; FILE REFERENCE: 266426USOXICP  
;; CURRENT APPLICATION NUMBER: US/11/065,943  
;; CURRENT FILING DATE: 2005-02-25  
;; PRIOR APPLICATION NUMBER: US 10/787,219  
;; PRIOR FILING DATE: 2004-02-27  
;; NUMBER OF SEQ ID NOS: 106  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 53  
;; LENGTH: 399  
;; TYPE: PRT  
;; ORGANISM: Bordetella pertussis  
US-11-065-943-53

Query Match 100.0%; Score 24; DB 7; Length 399;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
|||||  
Db 283 LNRRRA 287

RESULT 11  
US-11-055-822-336  
;; Sequence 336, Application US/11055822  
;; Publication No. US20050260707A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Pompejus, Markus  
;; APPLICANT: Kroger, Burkhard  
;; APPLICANT: Schroder, Hartwig  
;; APPLICANT: Zelder, Oskar  
;; APPLICANT: Haberhauer, Gregor  
;; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
;; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS  
;; FILE REFERENCE: BGI-121CPCN  
;; CURRENT APPLICATION NUMBER: US/11/055,822  
;; CURRENT FILING DATE: 2005-02-11  
;; PRIOR APPLICATION NUMBER: 09/606,740  
;; PRIOR FILING DATE: 2000-06-23  
;; PRIOR APPLICATION NUMBER: 60/141,031  
;; PRIOR FILING DATE: 1999-06-25  
;; PRIOR APPLICATION NUMBER: 60/142,101  
;; PRIOR FILING DATE: 1999-07-02  
;; PRIOR APPLICATION NUMBER: 60/148,613  
;; PRIOR FILING DATE: 1999-08-12  
;; PRIOR APPLICATION NUMBER: 60/187,970  
;; PRIOR FILING DATE: 2000-03-09  
;; PRIOR APPLICATION NUMBER: DE 19930476.9  
;; PRIOR FILING DATE: 1999-07-01  
;; PRIOR APPLICATION NUMBER: DE 19931415.2  
;; PRIOR FILING DATE: 1999-07-08  
;; PRIOR APPLICATION NUMBER: DE 19931418.7  
;; PRIOR FILING DATE: 1999-07-08  
;; PRIOR APPLICATION NUMBER: DE 19931419.5  
;; PRIOR FILING DATE: 1999-07-08  
;; PRIOR APPLICATION NUMBER: DE 19931420.9  
;; PRIOR FILING DATE: 1999-07-08  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 1158  
;; SEQ ID NO 336  
;; LENGTH: 401  
;; TYPE: PRT  
;; ORGANISM: Corynebacterium glutamicum

US-11-055-822-336

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Query Match      100.0%; Score 24; DB 7; Length 401;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 LNRR 5  
243 LNRR 247

**RESULT 12**

```

US-11-120-308-64
; Sequence 64, Application US/11120308
; Publication No. US20060005277A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Forge, Charlie
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: CDNAS Encoding Polypeptides
; FILE REFERENCE: BB-1365 US NA
; CURRENT APPLICATION NUMBER: US/11/120,308
; CURRENT FILING DATE: 2005-05-02
; PRIOR APPLICATION NUMBER: US/10/078,770

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, PRIOR FILING DATE: 2002-02-15
, PRIOR APPLICATION NUMBER: 09/614,188
, PRIOR FILING DATE: 2000-07-12
, PRIOR APPLICATION NUMBER: 60/143,400
, PRIOR FILING DATE: 1999-07-12
, PRIOR APPLICATION NUMBER: 60/153,534
, PRIOR FILING DATE: 1999-09-13
, PRIOR APPLICATION NUMBER: 60/161,223
, PRIOR FILING DATE: 1999-10-22
, PRIOR APPLICATION NUMBER: 60/159,878
, PRIOR FILING DATE: 1999-10-15
, PRIOR APPLICATION NUMBER: 60/157,401
, PRIOR FILING DATE: 1999-10-01
, PRIOR APPLICATION NUMBER: 60/143,419
, PRIOR FILING DATE: 1999-07-12
, PRIOR APPLICATION NUMBER: 60/143,409
, PRIOR FILING DATE: 1999-07-12
, NUMBER OF SEQ ID NOS: 196
, SOFTWARE: Microsoft Office 97
, SEQ ID NO 64
, LENGTH: 421
, TYPE: PRNT
, ORGANISM: Zea mays
US-11-120-308-64

```

Query Match 100.0%; Score 24; DB 7; Length 421;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRRA 5  
185 LNRRRA 189

## RESULT 13

US-11-102-240-134  
 ; Sequence 134, Application US/11102240  
 ; Publication No. US20050260647A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS  
 ; TITLE OF INVENTION: ESOPHAGEAL TUMOR  
 ; FILE REFERENCE: P3230R1C106C  
 ; CURRENT APPLICATION NUMBER: US/11/102,240  
 ; CURRENT FILING DATE: 2005-04-08

```

, PRIOR APPLICATION NUMBER: 10/063662
, PRIOR FILING DATE: 2002-05-07
, PRIOR APPLICATION NUMBER: 10/006867
, PRIOR FILING DATE: 2001-12-06
, PRIOR APPLICATION NUMBER: PCT/US00/23328
, PRIOR FILING DATE: 2000-08-24
, PRIOR APPLICATION NUMBER: 60/170262
, PRIOR FILING DATE: 199-12-09
, NUMBER OF SEQ ID NOS: 170
, SEQ ID NO 134
, LENGTH: 440
, TYPE: PRT
, ORGANISM: Homo Sapien
US-11-102-240-134

```

Query Match 100.0%; Score 24; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 5; Conservative 0; Mismatches 0; Indels

QY 1 LNRRRA 5  
272 LNRRRA 276

## RESULT 14

```

US-10-467-657-9140
; Sequence 9140, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9140
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9140

```

Query Match 91.7%; Score 22; DB 6; Length 164;  
Best Local Similarity 80.0%; Pred. No. 76;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	LNRRRA	5
		:	
Dp	13	INRRRA	17

RESULT 15

```

US-10-467-657-916
; Sequence 916, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12

```

```
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 916
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-916
```

```
Query Match      91.7%; Score 22; DB 6; Length 229;
Best Local Similarity 80.0%; Pred. NO. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 INRRA 5
       :||||
Db      18 INRRA 22
```

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Search completed: January 12, 2006, 16:35:20
Job time : 15.5 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2006, 16:18:51 ; Search time 86 Seconds  
(without alignments)  
24.292 Million cell updates/sec

Title: US-10-716-030-1  
Perfect score: 24  
Sequence: 1 LNRRRA 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications\_AA\_Main:\*
- 1: /cgn2.6/ptodata1/pubpaa/US07\_PUBCOMB.pgp:\*\*
  - 2: /cgn2.6/ptodata1/pubpaa/US08\_PUBCOMB.pgp:\*\*
  - 3: /cgn2.6/ptodata1/pubpaa/US09\_PUBCOMB.pgp:\*\*
  - 4: /cgn2.6/ptodata1/pubpaa/US10A\_PUBCOMB.pgp:\*\*
  - 5: /cgn2.6/ptodata1/pubpaa/US10B\_PUBCOMB.pgp:\*\*
  - 6: /cgn2.6/ptodata1/pubpaa/US11\_PUBCOMB.pgp:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	7	US-10-405-339-40	Sequence 40, Appl
2	24	100.0	11	US-10-617-876-29	Sequence 29, Appl
3	24	100.0	14	US-10-617-876-102	Sequence 102, Appl
4	24	100.0	17	US-10-272-411-47	Sequence 47, Appl
5	24	100.0	17	US-10-272-328A-47	Sequence 47, Appl
6	24	100.0	19	US-10-119-621-9	Sequence 9, Appli
7	24	100.0	19	US-10-264-844-9	Sequence 9, Appli
8	24	100.0	19	US-10-265-344-9	Sequence 9, Appli
9	24	100.0	19	US-10-265-451-9	Sequence 9, Appli
10	24	100.0	19	US-10-264-844-9	Sequence 9, Appli
11	24	100.0	32	US-10-029-386-32371	Sequence 32371, A
12	24	100.0	36	US-10-050-704-222	Sequence 222, App
13	24	100.0	36	US-10-798-512-222	Sequence 222, App
14	24	100.0	51	US-10-275-589-11	Sequence 11, Appl
15	24	100.0	51	US-10-019-065A-2	Sequence 2, Appli
16	24	100.0	51	US-10-437-963-131854	Sequence 131854,
17	24	100.0	51	US-10-874-850-2	Sequence 2, Appli
18	24	100.0	52	US-10-449-831A-234	Sequence 234, App
19	24	100.0	62	US-10-425-115-331778	Sequence 331778,
20	24	100.0	63	US-10-425-115-366584	Sequence 366584,
21	24	100.0	70	US-09-864-408A-7076	Sequence 7076, Ap
22	24	100.0	71	US-10-286-696-20	Sequence 20, Appl
23	24	100.0	71	US-10-890-368-20	Sequence 20, Appl
24	24	100.0	71	US-10-889-948-20	Sequence 20, Appl
25	24	100.0	73	US-10-437-963-188160	Sequence 188160,
26	24	100.0	73	US-10-425-115-201422	Sequence 201422,
27	24	100.0	74	US-10-767-701-62884	Sequence 62884, A

28	24	100.0	80	4	US-10-425-114-41490	Sequence 41490, A
29	24	100.0	80	4	US-10-425-115-231629	Sequence 231629,
30	24	100.0	82	4	US-10-319-799-72	Sequence 72, Appl
31	24	100.0	84	4	US-10-425-115-295879	Sequence 295879,
32	24	100.0	87	3	US-09-864-408A-7852	Sequence 7852, Ap
33	24	100.0	92	4	US-10-050-704-226	Sequence 226, App
34	24	100.0	92	4	US-10-798-512-226	Sequence 226, App
35	24	100.0	94	4	US-10-425-115-307564	Sequence 307564,
36	24	100.0	95	4	US-10-437-963-173068	Sequence 173068,
37	24	100.0	99	4	US-10-008-524A-133	Sequence 133, App
38	24	100.0	99	4	US-10-350-719-133	Sequence 133, App
39	24	100.0	100	4	US-10-437-963-137984	Sequence 137984,
40	24	100.0	100	4	US-10-425-115-271761	Sequence 271761,
41	24	100.0	102	3	US-09-746-783-21	Sequence 21, Appl
42	24	100.0	104	3	US-09-911-777-5	Sequence 5, Appli
43	24	100.0	104	4	US-10-045-574A-5	Sequence 5, Appli
44	24	100.0	104	6	US-11-016-922-5	Sequence 5, Appli
45	24	100.0	104	6	US-11-080-973-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1  
US-10-405-339-40  
; Sequence 40, Application US/10405339  
; Publication No. US20030190364A1  
; GENERAL INFORMATION:  
; APPLICANT: Panitch, Alyssa  
; APPLICANT: Seal, Brandon  
; TITLE OF INVENTION: Biological Affinity Based Delivery Systems  
; FILE REFERENCE: 9138-0079US  
; CURRENT APPLICATION NUMBER: US/10/405,339  
; CURRENT FILING DATE: 2003-04-01  
; PRIOR APPLICATION NUMBER: US 60/369,568  
; PRIOR FILING DATE: 2002-04-01  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 40  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-10-405-339-40

Query Match 100.0%; Score 24; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
|||||  
Db 1 LNRRRA 5

RESULT 2  
US-10-617-876-29  
; Sequence 29, Application US/10617876  
; Publication No. US20040076611A1  
; GENERAL INFORMATION:  
; APPLICANT: Bachmann, Martin F  
; APPLICANT: Tissot, Alain  
; APPLICANT: Pumps, Paul  
; APPLICANT: Cielens, Indulis  
; APPLICANT: Renhofa, Regina  
; TITLE OF INVENTION: Molecular Antigen Arrays  
; FILE REFERENCE: 1700.0310001  
; CURRENT APPLICATION NUMBER: US/10/617,876  
; CURRENT FILING DATE: 2003-07-14  
; PRIOR APPLICATION NUMBER: US 60/396,126  
; PRIOR FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: Patentin version 3.2

; SEQ ID NO 29  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-617-876-29

Query Match 100.0%; Score 24; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRRA 5  
Db 5 LNRRRA 9

RESULT 3  
US-10-617-876-102  
; Sequence 102, Application US/10617876  
; Publication No. US20040076611A1  
; GENERAL INFORMATION:  
; APPLICANT: Bachmann, Martin F  
; APPLICANT: Tisseot, Alain  
; APPLICANT: Pumpens, Paul  
; APPLICANT: Cielens, Indulis  
; APPLICANT: Renhofs, Regina  
; TITLE OF INVENTION: Molecular Antigen Arrays  
; FILE REFERENCE: 1700.0310001  
; CURRENT APPLICATION NUMBER: US/10/617,876  
; PRIOR FILING DATE: 2003-07-14  
; PRIOR FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 102  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: C-TNF-a mutant  
US-10-617-876-102

Query Match 100.0%; Score 24; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRRA 5  
Db 8 LNRRRA 12

RESULT 4  
US-10-272-411-47  
; Sequence 47, Application US/10272411  
; Publication No. US20030100068A1  
; GENERAL INFORMATION:  
; APPLICANT: Barnes Jewish Hospital  
; APPLICANT: Lam, Jonathan  
; APPLICANT: Ross, F. Patrick  
; APPLICANT: Teitelbaum, Steven  
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF  
; FILE REFERENCE: 60019620-0202  
; CURRENT APPLICATION NUMBER: US/10/272,411  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: 60/329,393  
; PRIOR FILING DATE: 2001-10-15  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 47  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-272-411-47

Query Match 100.0%; Score 24; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 87;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRRA 5  
Db 11 LNRRRA 15

RESULT 5  
US-10-272-328A-47  
; Sequence 47, Application US/10272328A  
; Publication No. US20030109444A1  
; GENERAL INFORMATION:  
; APPLICANT: Barnes Jewish Hospital  
; APPLICANT: Lam, Jonathan  
; APPLICANT: Ross, F. Patrick  
; APPLICANT: Teitelbaum, Steven  
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF  
; FILE REFERENCE: 60019620-0206  
; CURRENT APPLICATION NUMBER: US/10/272,328A  
; CURRENT FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: 60/329,393  
; PRIOR FILING DATE: 2001-10-15  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 47  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-272-328A-47

Query Match 100.0%; Score 24; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 87;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRRA 5  
Db 11 LNRRRA 15

RESULT 6  
US-10-119-621-9  
; Sequence 9, Application US/10119621  
; Publication No. US20030064021A1  
; GENERAL INFORMATION:  
; APPLICANT: RATHJEN, Deborah A  
; FERRANTE, Antonio  
; TITLE OF INVENTION: Neutrophil Stimulating Peptides  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER & WITCOFF, LTD. 3000  
; STREET: 10 S. Wacker Drive, Suite 3000  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: IBM compatible PC/MS-DOS  
; SOFTWARE: WordPerfect version 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/119,621  
; FILING DATE: 10-Apr-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/598,784  
; FILING DATE: 21-Jun-2000  
; APPLICATION NUMBER: AU PJ9065  
; FILING DATE: 12-MAR-1990  
; APPLICATION NUMBER: PCT/AU91/00086  
; FILING DATE: 12-MAR-1991

APPLICATION NUMBER: US 07/930,415  
FILING DATE: 09-NOV-1992  
APPLICATION NUMBER: US 08/107,235  
FILING DATE: 16-AUG-1993  
APPLICATION NUMBER: US 08/714,960  
FILING DATE: 17-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Resis, Robert H.  
REGISTRATION NUMBER: 32,168  
REFERENCE/DOCKET NUMBER: 11341.00001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 715-1000  
TELEFAX: (312) 715-1234  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..19  
OTHER INFORMATION: /note= "PEPTIDE 307 (22-40)"  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-119-621-9  
Query Match 100.0%; Score 24; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 97;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRA 5  
DB 8 LNRA 12

RESULT 7  
US-10-264-844-9  
; Sequence 9, Application US/10264844  
; Publication No. US20030139577A1  
; GENERAL INFORMATION:  
; APPLICANT: Rathjen, Deborah Ann  
; TITLE OF INVENTION: TUMOUR NECROSIS FACTOR BINDING LIGANDS  
; FILE REFERENCE: 27340202309  
; CURRENT APPLICATION NUMBER: US/10/264,844  
; CURRENT FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: US 09/736,630  
; PRIOR FILING DATE: 2000-12-13  
; PRIOR APPLICATION NUMBER: US 09/364,039  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: US 08/823,893  
; PRIOR FILING DATE: 1997-03-17  
; PRIOR APPLICATION NUMBER: US 08/344,133  
; PRIOR FILING DATE: 1994-11-23  
; PRIOR APPLICATION NUMBER: US 07/828,956  
; PRIOR FILING DATE: 1992-02-18  
; PRIOR APPLICATION NUMBER: PCT/AU90/00337  
; PRIOR FILING DATE: 1990-08-07  
; PRIOR APPLICATION NUMBER: AU PJ7576  
; PRIOR FILING DATE: 1989-11-24  
; PRIOR APPLICATION NUMBER: AU PJ5662  
; PRIOR FILING DATE: 1989-08-07  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct of amino acid residues 22-40  
; OTHER INFORMATION: from sequence of mature human tumor necrosis  
; OTHER INFORMATION: factor alpha

US-10-264-844-9  
Query Match 100.0%; Score 24; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 97;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRA 5  
DB 8 LNRA 12

RESULT 8  
US-10-265-344-9  
; Sequence 9, Application US/10265344  
; Publication No. US20030139580A1  
; GENERAL INFORMATION:  
; APPLICANT: Rathjen, Deborah Ann  
; APPLICANT: Aston, Roger  
; TITLE OF INVENTION: TUMOUR NECROSIS FACTOR BINDING LIGANDS  
; FILE REFERENCE: 27340202301  
; CURRENT APPLICATION NUMBER: US/10/265,344  
; CURRENT FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: US 09/736,630  
; PRIOR FILING DATE: 2000-12-13  
; PRIOR APPLICATION NUMBER: US 09/364,039  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: US 08/823,893  
; PRIOR FILING DATE: 1997-03-17  
; PRIOR APPLICATION NUMBER: US 08/344,133  
; PRIOR FILING DATE: 1994-11-23  
; PRIOR APPLICATION NUMBER: US 07/828,956  
; PRIOR FILING DATE: 1992-02-18  
; PRIOR APPLICATION NUMBER: PCT/AU90/00337  
; PRIOR FILING DATE: 1990-08-07  
; PRIOR APPLICATION NUMBER: AU PJ7576  
; PRIOR FILING DATE: 1989-11-24  
; PRIOR APPLICATION NUMBER: AU PJ5662  
; PRIOR FILING DATE: 1989-08-07  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct of amino acid residues 22-40  
; OTHER INFORMATION: from sequence of mature human tumor necrosis  
; OTHER INFORMATION: factor alpha

US-10-265-344-9  
Query Match 100.0%; Score 24; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 97;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRA 5  
DB 8 LNRA 12

RESULT 9  
US-10-265-451-9  
; Sequence 9, Application US/10265451  
; Publication No. US20030162948A1  
; GENERAL INFORMATION:  
; APPLICANT: Rathjen, Deborah Ann  
; APPLICANT: Aston, Roger  
; TITLE OF INVENTION: TUMOUR NECROSIS FACTOR BINDING LIGANDS  
; FILE REFERENCE: 27340202308  
; CURRENT APPLICATION NUMBER: US/10/265,451  
; CURRENT FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: US 09/736,630  
; PRIOR FILING DATE: 2000-12-13  
; PRIOR APPLICATION NUMBER: US 09/364,039

; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: US 08/823,893  
; PRIOR FILING DATE: 1997-03-17  
; PRIOR APPLICATION NUMBER: US 08/344,133  
; PRIOR FILING DATE: 1994-11-23  
; PRIOR APPLICATION NUMBER: US 07/828,956  
; PRIOR FILING DATE: 1992-02-18  
; PRIOR APPLICATION NUMBER: PCT/AU90/00337  
; PRIOR FILING DATE: 1999-08-07  
; PRIOR APPLICATION NUMBER: AU PJ7576  
; PRIOR FILING DATE: 1989-11-24  
; PRIOR APPLICATION NUMBER: AU PJ5662  
; PRIOR FILING DATE: 1989-08-07  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct of amino acid residues 22-40  
; OTHER INFORMATION: from sequence of mature human tumor necrosis  
; OTHER INFORMATION: factor alpha  
US-10-265-451-9

Query Match 100.0%; Score 24; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 97;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRRA 5  
Db 8 LNRRRA 12

RESULT 10  
US-10-264-844-9  
; Sequence 9, Application US/10264844  
; Publication No. US20040214993A2  
; GENERAL INFORMATION:  
; APPLICANT: Rathjen, Deborah Ann  
; APPLICANT: Aston, Roger  
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR BINDING LIGANDS  
; FILE REFERENCE: 273402002309  
; CURRENT APPLICATION NUMBER: US/10/264,844  
; CURRENT FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: US 09/736,630  
; PRIOR FILING DATE: 2000-12-13  
; PRIOR APPLICATION NUMBER: US 09/364,039  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: US 08/823,893  
; PRIOR FILING DATE: 1997-03-17  
; PRIOR APPLICATION NUMBER: US 08/344,133  
; PRIOR FILING DATE: 1994-11-23  
; PRIOR APPLICATION NUMBER: US 07/828,956  
; PRIOR FILING DATE: 1992-02-18  
; PRIOR APPLICATION NUMBER: PCT/AU90/00337  
; PRIOR FILING DATE: 1999-08-07  
; PRIOR APPLICATION NUMBER: AU PJ7576  
; PRIOR FILING DATE: 1989-11-24  
; PRIOR APPLICATION NUMBER: AU PJ5662  
; PRIOR FILING DATE: 1989-08-07  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct of amino acid residues 22-40  
; OTHER INFORMATION: from sequence of mature human tumor necrosis  
; OTHER INFORMATION: factor alpha  
US-10-264-844-9

Query Match 100.0%; Score 24; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 97;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRRA 5  
Db 8 LNRRRA 12

RESULT 11  
US-10-029-386-32371  
; Sequence 32371, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 32371  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL117187.3  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.5  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.6  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8  
US-10-029-386-32371

Query Match 100.0%; Score 24; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRRA 5  
Db 24 LNRRRA 28

RESULT 12  
US-10-050-704-222  
; Sequence 222, Application US/10050704  
; Publication No. US20030050442A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 62 Human Secreted Proteins  
; FILE REFERENCE: P2039P1  
; CURRENT APPLICATION NUMBER: US/10/050,704  
; CURRENT FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: 09/684,524  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: PCT/US00/08979  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: 60/128,693  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 60/130,991  
; PRIOR FILING DATE: 1999-04-26  
; NUMBER OF SEQ ID NOS: 344  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 222  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-050-704-222

Query Match 100.0%; Score 24; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRA 5  
Db 30 LNRA 34

RESULT 13

US-10-798-512-222  
; Sequence 222, Application US/10798512  
; Publication No. US20040152164A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 62 Human Secreted Proteins  
; FILE REFERENCE: P2039P1  
; CURRENT APPLICATION NUMBER: US/10/798,512  
; PRIOR FILING DATE: 2004-03-12  
; PRIOR APPLICATION NUMBER: US/09/684,524  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: PCT/US00/08979  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 60/128,693  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 60/130,991  
; PRIOR FILING DATE: 1999-04-26  
; NUMBER OF SEQ ID NOS: 344  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 222  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-798-512-222

Query Match 100.0%; Score 24; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRA 5  
Db 30 LNRA 34

RESULT 14

US-10-275-589-11  
; Sequence 11, Application US/10275589  
; Publication No. US20040023864A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubois-Stringfellow, Nathalie  
; APPLICANT: Steve, Rocznik  
; APPLICANT: Zolotarev, Aliya  
; TITLE OF INVENTION: Method of Regulating Angiogenesis Using RYK Protein  
; FILE REFERENCE: MSB 7266  
; CURRENT APPLICATION NUMBER: US/10/275,589  
; CURRENT FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: US 09/568,783  
; PRIOR FILING DATE: 2000-05-11  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 11  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: ARTIFICIAL  
; FEATURE:  
; OTHER INFORMATION: Illustrative random sequence  
US-10-275-589-11

Query Match 100.0%; Score 24; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRA 5  
Db 19 LNRA 23

RESULT 15

US-10-019-065A-2  
; Sequence 2, Application US/10019065A  
; Publication No. US20040086501A1  
; GENERAL INFORMATION:  
; APPLICANT: Bayer Corporation  
; TITLE OF INVENTION: Protein Having Activity As An Angiogenesis Modulator  
; FILE REFERENCE: MSB-7265-PCT  
; CURRENT APPLICATION NUMBER: US/10/019,065A  
; CURRENT FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: US 60/266,300  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Random sequence  
US-10-019-065A-2

Query Match 100.0%; Score 24; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRA 5  
Db 19 LNRA 23

Search completed: January 12, 2006, 16:34:38  
Job time : 87 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 12, 2006, 16:10:35 ; Search time 65 Seconds  
(without alignments)  
54.271 Million cell updates/sec

Title: US-10-716-030-1  
Perfect score: 24  
Sequence: 1 LNRRRA 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 70528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_treml.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	60	Q08090	SYNSP
2	24	100.0	72	Q853W6	9CAUD
3	24	100.0	86	Q5P816	AZOSE
4	24	100.0	96	Q7Q4A8	ANOCA
5	24	100.0	97	Q8FE20	ECOL6
6	24	100.0	98	Q8VUX4	STAHU
7	24	100.0	98	Q9LBE5	STAAU
8	24	100.0	98	Q6GD55	STAAU
9	24	100.0	98	Q5HJV3	STAAC
10	24	100.0	100	HIS1	KLEPN
11	24	100.0	109	Q5YXR3	NOCPA
12	24	100.0	110	Q9FSL4	BRUJA
13	24	100.0	114	Q6F4B4	TRASC
14	24	100.0	117	Q4P9X2	USTMA
15	24	100.0	117	Q9P071	HUMAN
16	24	100.0	118	Q4LIG1	9CAUD
17	24	100.0	121	Q7I170	LACDL
18	24	100.0	124	Q6F4B3	TRASC
19	24	100.0	138	Q9TTG7	AOTLE
20	24	100.0	138	Q4S586	TETNG
21	24	100.0	139	Q7XYL8	CHLS6
22	24	100.0	139	Q7NFX2	GLOVI
23	24	100.0	143	Q5IYE7	MAGGR
24	24	100.0	144	Q4UXC3	XANCP
25	24	100.0	144	Q87E25	XYLFT
26	24	100.0	144	Q9PGW4	XYLEA
27	24	100.0	144	Q8PE77	XANCP
28	24	100.0	145	Q5LQC4	SILPO
29	24	100.0	147	Q602F2	METCA
30	24	100.0	148	Q8SWQ2	ENCUC
31	24	100.0	149	Q97538	AOTVO

32	24	100.0	149	2	Q97543	AOTNA	Q97543	aotus nancy
33	24	100.0	149	2	Q9TIG8	AOTNI	Q9TIG8	aotus nigri
34	24	100.0	150	2	Q8LRS2	SORAU	Q8LRS2	sorbus aucu
35	24	100.0	155	2	Q8HZD5	SAGOE	Q8HZD5	saguinus oe
36	24	100.0	155	2	Q8HZD7	PONPY	Q8HZD7	pongo pygma
37	24	100.0	155	2	Q8HZD8	9PRIM	Q8HZD8	gorilla gor
38	24	100.0	156	2	Q4TJP7	9SPHN	Q4TJP7	erythroba
39	24	100.0	157	2	Q5NUW1	9BURK	Q5NUW1	raletonia m
40	24	100.0	158	2	Q4NU46	9MICC	Q4NU46	arthrobact
41	24	100.0	158	2	Q6MM44	BDEBA	Q6MM44	bdellovibri
42	24	100.0	161	2	Q4PNZ2	GLOAC	Q4PNZ2	glomerella
43	24	100.0	169	2	Q6DQL8	MAIZE	Q6DQL8	zea mays (m
44	24	100.0	173	2	Q6F9C6	ACIAD	Q6F9C6	acinetobact
45	24	100.0	179	2	Q7XJ85	PYRGO	Q7XJ85	pyrus commu

ALIGNMENTS

RESULT 1  
Q08090 SYNSP PRELIMINARY; PRT; 60 AA.  
AC Q08090;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE CpeB, cpeA genes and ORF3 (Fragment).  
OS Synechococcus sp.  
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.  
OX NCBI\_TaxID:1131;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=94207193; PubMed=7512390;  
RA Newman J., Mann N.H., Carr N.G.;  
RT "Organization and transcription of the class I phycoerythrin genes of  
RT the marine cyanobacterium Synechococcus sp. WH7803.";  
RL Plant Mol. Biol. 24:679-683(1994).  
DR EMBL; X72961; CAA51463.1; -, Genomic\_DNA.  
DR FIR; S43777; S43777.  
FT NON TER 60  
SQ SEQUENCE 60 AA; 6678 MW; 8773BCE2B82BECAC CRC64;

Query Match 100.0%; Score 24; DB 2; Length 60;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
|||  
DB 20 LNRRRA 24

RESULT 2  
Q853W6 9CAUD PRELIMINARY; PRT; 72 AA.  
ID Q853W6;  
AC Q853W6;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp200.  
GN Name=200;  
OS Mycobacteriophage Omega.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.  
OX NCBI\_TaxID=205879;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22592660; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2;  
RA Pedulla M.L., Ford M.B., Houtz J.M., Kartikeyan T., Wadsworth C.,  
RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Panunzio N.R.,  
RA Brucker W., Kumar V., Kandamany J., Keenan L., Bardarov S.,  
RA Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,  
RA Hatfull G.F.;  
RT "Origins of highly mosaic mycobacteriophage genomes.";  
RL Cell 113:171-182(2003).



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DR EMBL; AY129338; AAN12842.1; -; Genomic DNA.
SQ SEQUENCE 72 AA; 8042 MW; A38DAC1C5529B6F1 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRR 5
DB 16 LNRR 20

RESULT 3
QSP816 AZOSE
ID QSP816_AZOSE PRELIMINARY; PRT; 86 AA.
AC QSP816;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DE 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=AZOSEA04230; ORFNames=eba808;
OS Azococcus sp. (strain EbN1).
OC Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales;
OC Rhodocyclaceae; Azococcus.
OX NCBI_TaxID=76114;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=EBN1;
RX PubMed15551059; DOI=10.1007/s00203-004-0742-9;
RA Rabus R., Kube M., Heider J., Beck A., Heitmann K., Widdel P.,
RA Reinhardt R.;
RT "The genome sequence of an anaerobic aromatic-degrading denitrifying
bacterium, strain EbN1."
RL Arch. Microbiol. 183:27-36(2005).
DR EMBL; CR555306; CAI06545.1; -; Genomic DNA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 86 AA; 9410 MW; ADA604AEFFB8CF CRC64;

Query Match 100.0%; Score 24; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRR 5
DB 12 LNRR 16

RESULT 4
Q7Q4A8 ANOGA
ID Q7Q4A8_ANOGA PRELIMINARY; PRT; 96 AA.
AC Q7Q4A8;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE ENSANGP00000018223.
GN ORFNames=ENSANGG00000015734;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation."
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;

DR EMBL; AY129338; AAN12842.1; -; Genomic DNA.
SQ SEQUENCE 72 AA; 8042 MW; A38DAC1C5529B6F1 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRR 5
DB 16 LNRR 20

RESULT 3
QSP816 AZOSE
ID QSP816_AZOSE PRELIMINARY; PRT; 86 AA.
AC QSP816;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DE 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=AZOSEA04230; ORFNames=eba808;
OS Azococcus sp. (strain EbN1).
OC Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales;
OC Rhodocyclaceae; Azococcus.
OX NCBI_TaxID=76114;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=EBN1;
RX PubMed15551059; DOI=10.1007/s00203-004-0742-9;
RA Rabus R., Kube M., Heider J., Beck A., Heitmann K., Widdel P.,
RA Reinhardt R.;
RT "The genome sequence of an anaerobic aromatic-degrading denitrifying
bacterium, strain EbN1."
RL Arch. Microbiol. 183:27-36(2005).
DR EMBL; CR555306; CAI06545.1; -; Genomic DNA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 86 AA; 9410 MW; ADA604AEFFB8CF CRC64;

Query Match 100.0%; Score 24; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRR 5
DB 12 LNRR 16

RESULT 4
Q7Q4A8 ANOGA
ID Q7Q4A8_ANOGA PRELIMINARY; PRT; 96 AA.
AC Q7Q4A8;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE ENSANGP00000018223.
GN ORFNames=ENSANGG00000015734;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation."
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;

RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008964; EAA12199.2; -; Genomic DNA.
DR InterPro; IPR001562; BTK.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011993; PH type.
DR PROSITE; PS50003; PH DOMAIN; 1.
DR PROSITE; PS1113; ZF-BTK; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 96 AA; 11216 MW; 6ECE774DC9CBCE26 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRR 5
DB 68 LNRR 72

RESULT 5
Q8FE20 ECOL6
ID Q8FE20_ECOL6 PRELIMINARY; PRT; 97 AA.
AC Q8FE20;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein c3549.
GN OrderedLocusNames=c3549;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=O6:H1 / CPT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rayko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli."
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR EMBL; AB016766; AAN81997.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 97 AA; 10945 MW; 138DBF80ACF67E5 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRR 5
DB 91 LNRR 95

RESULT 6
Q8VUX4 STAHO
ID Q8VUX4_STAHO PRELIMINARY; PRT; 98 AA.
AC Q8VUX4;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE ORF12.
OS Staphylococcus hominis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GIFU12263;

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RX MEDLINE=22586405; PubMed=12700250;
RX DOI=10.1128/JB.185.9.2711-2722.2003;
RA Katayama Y., Takeuchi F., Ito T., Ma X.X., Ui-Mizutani Y.,
RA Kobayashi I., Hiramatsu K.;
RT "Identification in methicillin-susceptible Staphylococcus hominis of
RT an active primordial mobile genetic element for the staphylococcal
RT cassette chromosome mec of methicillin-resistant Staphylococcus
RT aureus.";
RL J. Bacteriol. 185:2711-2722(2003).
DR EMBL: AB063171; BAB83483.1; -; Genomic_DNA.
DR InterPro: IPR010813; DUF1413.
DR Pfam: PF07205; DUF1413; 1.
SQ SEQUENCE 98 AA; 11104 MW; 2B95AB85279039C9 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5
Db 34 LNRRRA 38

RESULT 7
Q9LBZ5 STAAU PRELIMINARY; PRT; 98 AA.
ID Q9LBZ5 STAAU PRELIMINARY; PRT; 98 AA.
AC Q9LBZ5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP STRAIN=NCTC10442;
RC MEDLINE=21199321; PubMed=11302791;
RX DOI=10.1128/JAC.45.5.1323-1336.2001;
RA Ito T., Katayama Y., Asada K., Mori N., Tautumimoto K.;
RT "Structural comparison of three types of staphylococcal cassette
RT chromosome mec integrated in the chromosome in methicillin-resistant
RT Staphylococcus aureus.";
RL Antimicrob. Agents Chemother. 45:1323-1336(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCTC10442;
RA Ito T., Okuma K., Xue M.X., Yuzawa H., Hiramatsu K.;
RT "Insights on antibiotic resistance of Staphylococcus aureus from its
RT whole genome: genomic island SCC.";
RL Drug Resist. Updat. 6:41-52(2003).
DR EMBL: AB033763; BAA94325.1; -; Genomic_DNA.
DR InterPro: IPR010813; DUF1413.
DR Pfam: PF07205; DUF1413; 1.
KW Hypothetical protein.
SQ SEQUENCE 98 AA; 11149 MW; DCCF9B59FFFAE0A CRC64;

Query Match 100.0%; Score 24; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5
Db 34 LNRRRA 38

RESULT 8
Q6GD55 STAAU PRELIMINARY; PRT; 98 AA.
ID Q6GD55 STAAU PRELIMINARY; PRT; 98 AA.
AC Q6GD55;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

```

```

DE Hypothetical protein.
GN OrderedLocusNames=SAS0035;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL: BX571857; CAG41807.1; -; Genomic_DNA.
DR InterPro: IPR010813; DUF1413.
DR Pfam: PF07205; DUF1413; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 98 AA; 11109 MW; 8D5577B576DE82C6 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5
Db 34 LNRRRA 38

RESULT 9
Q5HJV3 STAAU PRELIMINARY; PRT; 98 AA.
ID Q5HJV3 STAAU PRELIMINARY; PRT; 98 AA.
AC Q5HJV3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=SACOL0044;
OS Staphylococcus aureus (strain COL).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=93062;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;
RA Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,
RA Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,
RA Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
RA Haft D.H., Vamathevan J.J., Khouri H., Utterback T.R., Lee C.,
RA Dmitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,
RA Hance I.R., Nelson K.B., Fraser C.M.;
RT "Insights on evolution of virulence and resistance from the complete
RT genome analysis of an early methicillin-resistant Staphylococcus
RT aureus strain and a biofilm-producing methicillin-resistant
RT Staphylococcus epidermidis strain.";
RL J. Bacteriol. 187:2426-2438(2005).
DR EMBL: CP000046; AAW38693.1; -; Genomic_DNA.
DR TIGR: SACOL0044;
DR InterPro: IPR010813; DUF1413.
DR Pfam: PF07205; DUF1413; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 98 AA; 11149 MW; DCCF9B59FFFAE0A CRC64;

Query Match 100.0%; Score 24; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5

```

```

Db          34 LNRR 38
|||||
ID HIS1_KLEPN STANDARD; PRT; 100 AA.
AC P05148;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE ATP phosphoribosyltransferase (EC 2.4.2.17) (ATP-PRTase) (ATP-PRT)
DE (Fragment)
GN Name=hisG;
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=84135578; PubMed=6321433;
RA Rodriguez R.L., West R.W. Jr.;
RT "Histidine operon control region of Klebsiella pneumoniae: analysis
RT with an Escherichia coli promoter-probe plasmid vector.";
RL J. Bacteriol. 157:764-771(1984).
CC -|- FUNCTION: Catalyzes the condensation of ATP and PRPP to form N'-
CC 5'-phosphoribosyl-ATP (PR-ATP). Has a crucial role in the pathway
CC because the rate of histidine biosynthesis seems to be controlled
CC primarily by regulation of hisG enzymatic activity (By
CC similarity).
CC -|- CATALYTIC ACTIVITY: 1-(5-phospho-D-ribose)-ATP + diphosphate =
CC ATP + 5-phospho-alpha-D-ribose 1-diphosphate.
CC -|- COFACTOR: Magnesium (By similarity).
CC -|- ENZYME REGULATION: Feedback inhibited by histidine (By
CC similarity).
CC -|- PATHWAY: Amino-acid biosynthesis; L-histidine biosynthesis; L-
CC histidine from PRPP; step 1.
CC -|- SUBUNIT: Equilibrium between an active dimeric form, an inactive
CC hexameric form and higher aggregates. Interconversion between the
CC various forms is largely reversible and is influenced by the
CC natural substrates and inhibitors of the enzyme (By similarity).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- SIMILARITY: Belongs to the ATP phosphoribosyltransferase family.
CC Long subfamily.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR EMBL; K01997; AAA25073.1; -; Genomic_DNA.
DR SMR; P05148; 5-100.
DR HAMAP; MF_00079; -; 1.
DR InterPro; IPR001348; ATP_phospho_trans.
DR Pfam; PF01634; HisG; 1.
DR PROSITE; PS01316; ATP_P_PHORIBOSYLTR; PARTIAL.
KW Amino-acid biosynthesis; Glycosyltransferase; Histidine biosynthesis;
KW Magnesium; Metal-binding; Transferase.
FT NON TER 100 100
SQ SEQUENCE 100 AA; 11408 MW; BDA8FEB042E012DE CRC64;

Query Match 100.0%; Score 24; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRR 5
|||||
Db 82 LNRR 86

RESULT 11
QSYXR3_NOCFA

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```

ID QSYXR3_NOCFA PRELIMINARY; PRT; 109 AA.
AC QSYXR3;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Putative transcriptional regulator.
GN OrderedLocusNames=nfa21810;
OS Nocardia farcinica.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Nocardia.
OX NCBI_TaxID=37329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IFM 10152;
RX PubMed=15466710; DOI=10.1073/pnas.0406410101;
RA Ishikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K.,
RA Shiba T., Hattori M.;
RT "The complete genomic sequence of Nocardia farcinica IFM 10152.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
DR EMBL; AP006618; BAD57028.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; E:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001845; HTH ARSR.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF01022; HTH 5; 1.
DR PRINTS; PR00778; HTHARSR.
DR SMART; SM00418; HTH ARSR; 1.
DR PROSITE; PS50987; HTH ARSR_2; 1.
KW Cadmium resistance; Complete proteome; DNA-binding; Transcription;
KW Transcription regulation.
SQ SEQUENCE 109 AA; 12758 MW; C8B8C003FB725173 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRR 5
|||||
Db 73 LNRR 77

RESULT 12
QSF5L4_BRAJA
ID QSF5L4_BRAJA PRELIMINARY; PRT; 110 AA.
AC Q9F5L4; Q79U54;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE NapD (periplasmic nitrate reductase).
GN Name=napD; OrderedLocusNames=blr7037;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=110spc4;
RX PubMed=14663073; DOI=10.1099/mic.0.26620-0;
RA Delgado M., Bonnard N., Tresierra-Ayala A., Bedmar E.J., Muller P.;
RT "The Bradyrhizobium japonicum napEDABC genes encoding the periplasmic
RL nitrate reductase are essential for nitrate respiration.";
RL Microbiology 149:3395-3403(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=110spc4;
RA Mueller P.;
RT "The putative napD napA operon of Bradyrhizobium japonicum 110spc4.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=USDA 110;

```

RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Ideasa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197(2002).
DR EMBL; AF314590; AAG31647.1; -; Genomic\_DNA.
DR EMBL; BA000040; BACS2302.1; -; Genomic\_DNA.
DR InterPro; IPR005623; NapD.
DR Pfam; PF03927; NapD; 1.
KW Complete proteome.
SQ SEQUENCE 110 AA; 11787 MW; 9546CE2C46FC0BDB CRC64;

Query Match 100.0%; Score 24; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5
DB 12 LNRRRA 16

RESULT 13
ID Q6F4B4\_TRASC PRELIMINARY; PRT; 114 AA.
AC Q6F4B4\_
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Preproghrelin-1 precursor.
OS Trachemys scripta elegans.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemys.
OX NCBI\_TaxID=31138;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Stomach;
RC PubMed=15242751; DOI=10.1016/j.ygcen.2004.05.005;
RA Kaiya H., Sakata I., Kojima M., Hosoda H., Sakai T., Kangawa K.;
RT "Structural determination and histochemical localization of ghrelin in
RT the red-eared slider turtle, Trachemys scripta elegans."
RL Gen. Comp. Endocrinol. 138:50-57(2004).
DR EMBL; AB161457; BAD29730.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
DR InterPro; IPR005441; Preproghrelin.
DR PANTHER; PTHR14122; Preproghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD322162; Preproghrelin; 1.
KW Signal.
FT SIGNAL. 1 23 Potential.
FT CHAIN 24 48 ghrelin.
SQ SEQUENCE 114 AA; 13300 MW; 07DE5E24BF9DEDF2 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5
DB 47 LNRRRA 51

RESULT 14
ID Q4P9X2\_USTMA PRELIMINARY; PRT; 117 AA.
AC Q4P9X2\_
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Predicted protein.

GN ORFNames=UM03091.1;
OS Ustilago maydis 521.
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI\_TaxID=237631;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=521;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blitsheteyn B., Bloom T., Blye J., Boguclavsky L.,
RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshateang Y., Citroen M.,
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA Dorjee K., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Duffey N., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Gnrirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseles M., Karlsson E.,
RA Kella C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-ton K., Liu X., Lokytsang T., Lokytsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
RA Mesirov J., Mihalev A., Mihova T., Mikkelson T., Mieng V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
RA O'Neill K., Oman S., Parker S., Perrin D., Phunkhang P., Pignani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuang P.,
RA Tensing P., Tesfaye S., Theodore J., Thoultsang Y., Topham K.,
RA Towey S., Tsanla T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Zimmer A., Zody M., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Ustilago maydis."
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACP01000104; EAK83882.1; -; Genomic\_DNA.
SQ SEQUENCE 117 AA; 12734 MW; 357E4480E3118265 CRC64;

Query Match 100.0%; Score 24; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5
DB 93 LNRRRA 97

RESULT 15
ID Q9P071\_HUMAN PRELIMINARY; PRT; 117 AA.
AC Q9P071\_
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE HSPC311 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OX Homo.

RN NCBI\_TaxID=9606;

[1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Blood;

RA Ye M., Zhang Q.H., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,

RL Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;

DR EMBL; AF161429; AAF28989.1; -; mRNA.

FT NON TER 1

SQ SEQUENCE 117 AA; 13276 MW; 246F7F794620AAPP CRC64;

Query Match 100.0%; Score 24; DB 2; Length 117;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRR 5

Db 80 LNRRR 84

Search completed: January 12, 2006, 16:18:43

Job time : 67 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 12, 2006, 16:12:05 ; Search time 11.5 Seconds  
(without alignments)  
41.833 Million cell updates/sec

Title: US-10-716-030-1

Perfect score: 24

Sequence: 1 LNRRRA 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	60	2 S43777	hypothetical prote
2	24	100.0	122	2 E69980	hypothetical prote
3	24	100.0	144	2 H82837	conserved hypothet
4	24	100.0	189	2 S04670	hypothetical prote
5	24	100.0	194	2 JS0664	interferon precurs
6	24	100.0	233	1 QMHUN	tumor necrosis fac
7	24	100.0	233	1 S22052	tumor necrosis fac
8	24	100.0	237	2 C87856	GGDEF family prote
9	24	100.0	247	2 B87283	tRNA pseudouridine
10	24	100.0	255	2 AG3435	guanylate kinase (
11	24	100.0	259	2 G95890	probable transcrip
12	24	100.0	278	2 S77601	hypothetical prote
13	24	100.0	285	2 I38248	steroidogenic acut
14	24	100.0	285	2 JC4315	steroidogenic acut
15	24	100.0	287	2 F70788	hypothetical prote
16	24	100.0	299	1 XREBT	ATP phosphoribosyl
17	24	100.0	299	1 XREBT	ATP phosphoribosyl
18	24	100.0	299	2 AC0764	ATP phosphoribosyl
19	24	100.0	299	2 D90981	ATP phosphoribosyl
20	24	100.0	299	2 B85827	ATP phosphoribosyl
21	24	100.0	299	2 A10188	ATP phosphoribosyl
22	24	100.0	304	2 A13285	geranyltranstransf
23	24	100.0	306	2 AC2649	ABC transporter, m
24	24	100.0	310	2 I46987	bone sialoprotein
25	24	100.0	319	2 I60446	Shiga-like cytotox
26	24	100.0	325	2 D37476	fiber - human aden
27	24	100.0	337	2 B97431	alpha-glucosides t
28	24	100.0	338	2 T36307	hypothetical prote
29	24	100.0	341	2 T46153	hypothetical prote

yeast bud pattern  
steroidogenic acut  
conserved hypothet  
probable argg prot  
arginosuccinate sy  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
glucose-fructose o  
GGDEF family prote  
hypothetical prote  
probable membrane  
probable purine pe  
probable transport  
probable transport

ALIGNMENTS

RESULT 1

S43777

hypothetical protein 3 - Synchococcus sp.

C:Species: Synchococcus sp.

C>Date: 10-Dec-1994 #sequence\_revision 26-May-1995 #text\_change 05-Oct-2004

C:Accession: S43777; S32640

R:Newman, J.; Mann, N.H.; Carr, N.G.

Plant Mol. Biol. 24, 679-683, 1994

A:Title: Organization and transcription of the class I phycoerythrin genes of the marin

A:Reference number: S43777; MUID:94207193; PMID:7512390

A:Accession: S43777

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-60 <NEW>

A:Cross-references: UNIPROT:Q08090; UNIPARC:UPI00000B8C83; EMBL:X72961; NID:3288983; P1:

A:Note: the authors translated the codon CAC for residue 27 as His

C:Superfamily: uncharacterized conserved protein

Query Match 100.0%; Score 24; DB 2; Length 60;

Best Local Similarity 100.0%; Pred. No. 27;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 LNRRRA 5

|||||

20 LNRRRA 24

RESULT 2

E69980

hypothetical protein yrvB - Bacillus subtilis

C:Species: Bacillus subtilis

C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 15-Oct-1999

C:Accession: E69980

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte

C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A.; Ehrlich, S.D.; Emmerston, P.T.; Entian, K.D.; Errington, J.; Fabbet, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle

tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue

Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecell

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosa, V.; Uchiyama

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yamamoto, H.; Yamamoto, H.;

A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: E69980

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A;Residues: 1-122 <KUN>  
 A;Cross-references: UNIPARC:UPI000006082B; GB:Z99118; GB:AL009126; NID:G2635200; PIDN:CA  
 A;Experimental source: strain 168  
 C;Genetics:  
 A;Gene: yrvb

Query Match 100.0%; Score 24; DB 2; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 56;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
 |||||  
 Db 68 LNRRRA 72

RESULT 3  
 H82837  
 conserved hypothetical protein XF0184 [imported] - Xylella fastidiosa (strain 9a5c)  
 C;Species: Xylella fastidiosa  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
 C;Accession: H82837

R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
 Nature 406, 151-157, 2000  
 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A;Reference number: A82515; MUID:20365717; PMID:10910347  
 A;Note: for a complete list of authors see reference number A59328 below

A;Accession: H82837  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-144 <SIM>

A;Cross-references: UNIPROT:O9PGW4; UNIPARC:UPI00000C2313; GB:AE003872; GB:AE003849; NID  
 A;Experimental source: strain 9a5c  
 R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H  
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.  
 submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig  
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E  
 A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
 , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A  
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
 A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv  
 M.; Tuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
 A;Reference number: A59328  
 A;Contents: annotation  
 C;Genetics:  
 A;Gene: XF0184

Query Match 100.0%; Score 24; DB 2; Length 144;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
 |||||  
 Db 84 LNRRRA 88

RESULT 4  
 S04670  
 hypothetical protein 5 - Rhodopsudomonas blastica  
 C;Species: Rhodopsudomonas blastica  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
 C;Accession: S04670  
 R;Tybulewicz, V.L.J.; Falk, G.; Walker, J.R.  
 J. Mol. Biol. 179, 185-214, 1984  
 A;Title: Rhodopsudomonas blastica atp operon. Nucleotide sequence and transcription.  
 A;Reference number: S04666; MUID:85058188; PMID:6209404

A;Accession: S04670  
 A;Status: not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 1-189 <TYB>  
 A;Cross-references: UNIPROT:P05448; UNIPARC:UPI000013A168

Query Match 100.0%; Score 24; DB 2; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 88;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
 |||||  
 Db 5 LNRRRA 9

RESULT 5  
 JS0664  
 interferon precursor - cat  
 C;Species: Felis silvestris catus (domestic cat)  
 C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
 C;Accession: JS0664

R;Nakamura, N.; Sudo, T.; Matsuda, S.; Yanai, A.  
 Biosci. Biotechnol. Biochem. 56, 211-214, 1992  
 A;Title: Molecular cloning of feline interferon cDNA by direct expression.

A;Reference number: JS0664; MUID:92323151; PMID:1377975

A;Accession: JS0664

A;Molecule type: mRNA

A;Residues: 1-194 <NAK>

A;Cross-references: UNIPROT:P35849; UNIPARC:UPI000012D64A

C;Superfamily: interferon alpha

C;Keywords: glycoprotein

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-194/Product: interferon #status predicted <INT>

F;102/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 24; DB 2; Length 194;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
 |||||  
 Db 33 LNRRRA 37

RESULT 6

QMHUN

tumor necrosis factor alpha precursor [validated] - human

N;Alternate names: cachectin; TNFA

C;Species: Homo sapiens (man)

C;Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 09-Jul-2004

C;Accession: A93585; S36153; A93351; A4189; B61478; I53311; S62610; I54522; A01646; B23

R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, E

Nucleic Acids Res. 13, 6361-6373, 1985

A;Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chrc

A;Reference number: A93585; MUID:86016093; PMID:2995927

A;Accession: A93585

A;Molecule type: DNA

A;Residues: 1-233 <NED>

A;Cross-references: UNIPROT:P01375; UNIPARC:UPI000000D745; GB:X02910; GB:X02159; NID:G37

R;Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka

Nature Genet. 3, 137-145, 1993

A;Title: Dense Alu clustering and a potential new member of the NFkappaB family within a

A;Reference number: S36152; MUID:93272029; PMID:8499947

A;Accession: S36153

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-233 <IRT>

A;Cross-references: UNIPARC:UPI000000D745; EMBL:Z15026; NID:G37211; PIDN:CAA78745.1; PII

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992

R;Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.

Nature 312, 724-729, 1984

A;Title: Human tumour necrosis factor: precursor structure, expression and homology to l

A;Reference number: A93351; MUID:85086244; PMID:6392892

A;Accession: A93351

A;Molecule type: mRNA

A;Residues: 1-233 <PEN>

A;Cross-references: UNIPARC:UPI000000D745; GB:X02910; GB:X02159; NID:G37209; PIDN:CAA266

A;Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyeloc





C;Accession: E87283  
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; deBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonin, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A;Title: Complete Genome Sequence of *Caulobacter crescentus*.  
 A;Reference number: A87249; MUID:21173698; PMID:11259647  
 A;Accession: E87283  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-247 <STO>  
 A;Cross-references: UNIPROT:Q9ABF0; UNIPARC:UPI00000D4535; GB:AE005673; NID:gi3421415; H  
 C;Genetics:  
 A;Gene: CC0278  
 C;Superfamily: tRNA-pseudouridine synthase A, prokaryotic type

Query Match 100.0%; Score 24; DB 2; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRRA 5  
 |||||  
 Db 116 LNRRRA 120

RESULT 10  
 AG3435  
 guanylate kinase (SC 2.7.4.8) [imported] - *Brucella melitensis* (strain 16M)  
 C;Species: *Brucella melitensis*  
 C;Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002  
 C;Accession: AG3435  
 R;DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, .; Mazur, M.; Goltsman, E.; Selkov, E.; Elizer, P.H.; Hagijs, S.; O'Callaghan, D.; Letesse Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*  
 A;Reference number: AD3252; PMID:11756688  
 A;Accession: AG3435  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-255 <KUR>  
 A;Cross-references: UNIPARC:UPI00000580A3; GB:AE008917; PIDN:AAL52650.1; PID:gi7983473;  
 A;Experimental source: strain 16M  
 C;Genetics:  
 A;Gene: BME11469  
 A;Map position: 1  
 C;Keywords: phosphotransferase

Query Match 100.0%; Score 24; DB 2; Length 255;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRRA 5  
 |||||  
 Db 180 LNRRRA 184

RESULT 11  
 G95890  
 probable transcription regulator protein [imported] - *Sinorhizobium meliloti* (strain 102)  
 C;Species: *Sinorhizobium meliloti*  
 C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
 C;Accession: G95890  
 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
 A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo  
 A;Reference number: A95842; MUID:21396508; PMID:11481431  
 A;Accession: G95890  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-259 <KUR>  
 A;Cross-references: UNIPROT:Q92WE9; UNIPARC:UPI00000CB4F5; GB:AL591985; PIDN:CAC48791.1;  
 A;Experimental source: strain 1021, megaplasmid pSymB  
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.  
 Science 293, 668-672, 2001  
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wellis, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.  
 A;Reference number: A96039; MUID:21368234; PMID:11474104  
 A;Contents: annotation  
 C;Genetics:  
 A;Gene: SM520405  
 A;Genome: plasmid

Query Match 100.0%; Score 24; DB 2; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRRA 5  
 |||||  
 Db 82 LNRRRA 86

RESULT 12  
 S77601  
 hypothetical protein 278 - *Paracoccus denitrificans*  
 C;Species: *Paracoccus denitrificans*  
 C;Date: 24-Oct-1998 #sequence\_revision 24-Oct-1998 #text\_change 09-Jul-2004  
 C;Accession: S77601  
 R;de Gier, J.W.; Schepper, M.; Reijnders, W.N.M.; van Dyck, S.J.; Slotboom, D.J.; Warne, M.L. Microbiol. 20, 1247-1260, 1996  
 A;Title: Structural and functional analysis of aa(3)-type and cbb(3)-type cytochrome c  
 A;Reference number: S77595; MUID:96405647; PMID:8809776  
 A;Accession: S77601  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-278 <DEA>  
 A;Cross-references: UNIPROT:Q51678; UNIPARC:UPI00000AF7F3; EMBL:U34953; NID:g1002874; PI  
 A;Experimental source: strain Pd1222  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995

Query Match 100.0%; Score 24; DB 2; Length 278;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNRRRA 5  
 |||||  
 Db 232 LNRRRA 236

RESULT 13  
 I38248  
 steroidogenic acute regulatory protein - human  
 C;Species: *Homo sapiens* (man)  
 C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
 C;Accession: I38248; I38896  
 R;Sugawara, T.; Lin, D.; Holt, J.A.; Martin, K.O.; Javitt, N.B.; Miller, W.L.; Strauss, Biochemistry 34, 12506-12512, 1995  
 A;Title: Structure of the human steroidogenic acute regulatory protein (StAR) gene: SCAP  
 A;Reference number: I38248; MUID:96038208; PMID:7547998  
 A;Accession: I38248  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-285 <RES>  
 A;Cross-references: UNIPROT:P49675; UNIPARC:UPI000003AD93; EMBL:U29105; NID:g1041696; PI  
 R;Sugawara, T.; Holt, J.A.; Driscoll, D.; Strauss III, J.F.; Lin, D.; Miller, W.L.; Pat Proc. Natl. Acad. Sci. U.S.A. 92, 4778-4782, 1995  
 A;Title: Human steroidogenic acute regulatory protein: functional activity in COS-1 cell  
 A;Reference number: I38896; MUID:95281540; PMID:7761400  
 A;Accession: I38896  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-285 <RES>  
 A;Cross-references: UNIPARC:UPI000003AD93; EMBL:U17280; NID:g727252; PIDN:AAC50141.1; C;Genetics:

Search completed: January 12, 2006, 16:19:17  
Job time : 13.5 secs

A;Gene: StAR  
A;Cross-references: GDB:STAR; GDB:635457; OMIM:600617  
A;Map position: 8p11.2-8p11.2  
A;Introns: 22/1; 60/1; 102/3; 155/3; 217/2; 248/3

Query Match 100.0%; Score 24; DB 2; Length 285;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
|||  
Db 35 LNRRRA 39

## RESULT 14

JC4315  
steroidogenic acute regulatory protein - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004  
C;Accession: JC4315  
R;Hartung, S.; Rust, W.; Balvers, M.; Ivell, R.  
Biochem. Biophys. Res. Commun. 215, 646-653, 1995  
A;Title: Molecular cloning and in vivo expression of the bovine steroidogenic acute regu  
A;Reference number: JC4315; MUID:96011827; PMID:7488004  
A;Accession: JC4315  
A;Molecule type: mRNA  
A;Residues: 1-285 <HAR>  
A;Cross-references: UNIPROT:Q28918; UNIPARC:UPI0000136090  
C;Comment: This protein is an acute controller of the rate-limiting transfer of cholesterol  
C;Genetics:  
A;Gene: StAR  
F;226-264/Region: metalloproteinase-1 tissue inhibitor similarity

Query Match 100.0%; Score 24; DB 2; Length 285;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
|||  
Db 35 LNRRRA 39

## RESULT 15

F70788  
hypothetical protein Rv3661 - Mycobacterium tuberculosis (strain H37RV)  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 31-Dec-2004  
C;Accession: F70788  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A;Reference number: A70500; MUID:98295987; PMID:9634230  
A;Accession: F70788  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-287 <COL>  
A;Cross-references: UNIPROT:O69629; UNIPARC:UPI0000139267; GB:AL022121; GB:AL123456; NID  
A;Experimental source: strain H37RV  
C;Genetics:  
A;Gene: Rv3661  
C;Superfamily: phosphoserine phosphatase

Query Match 100.0%; Score 24; DB 2; Length 287;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNRRRA 5  
|||  
Db 55 LNRRRA 59

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